

WEST Search History

DATE: Thursday, May 27, 2004

Hide?	Set Name	Query	Hit Count
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L12	L9 .clm.	26
<input type="checkbox"/>	L11	L9 adj number	0
<input type="checkbox"/>	L10	L9 and l3	477
<input type="checkbox"/>	L9	209526	517
<input type="checkbox"/>	L8	Accession number 2090526	0
<input type="checkbox"/>	L7	wood-william-\$.in	0
<input type="checkbox"/>	L6	wood-william-\$.in	0
<input type="checkbox"/>	L5	gurney-austin-\$.in.	1827
<input type="checkbox"/>	L4	godowaski-paul-\$.in.	0
<input type="checkbox"/>	L3	goddard-audrey.in.	1871
<i>DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L2	Fivaroff-ellen.in.	0
<input type="checkbox"/>	L1	6642360.pn.	1

END OF SEARCH HISTORY

First Hit Fwd Refs
End of Result Set

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L1: Entry 1 of 1

File: USPT

Nov 4, 2003

US-PAT-NO: 6642360

DOCUMENT-IDENTIFIER: US 6642360 B2

TITLE: Secreted polypeptides that stimulate release of proteoglycans from cartilage

DATE-ISSUED: November 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Filvaroff; Ellen	San Francisco	CA		
Goddard; Audrey	San Francisco	CA		
Godowski; Paul J.	Burlingame	CA		
Grimaldi; J. Christopher	San Francisco	CA		
Gurney; Austin L.	Belmont	CA		
Wood; William I.	Hillsborough	CA		

US-CL-CURRENT: 530/350; 530/324

CLAIMS:

What is claimed is:

1. An isolated polypeptide having at least 80% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

2. The isolated polypeptide of claim 1 having at least 85% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

3. The isolated polypeptide of claim 1 having at least 90% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

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L1: Entry 1 of 1

File: USPT

Jan 28, 2003

US-PAT-NO: [6512095](#)

DOCUMENT-IDENTIFIER: US 6512095 B2

TITLE: Molecules designated B7L-1

DATE-ISSUED: January 28, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Baum; Peter R.	Seattle	WA		

US-CL-CURRENT: [530/350](#); [424/130.1](#), [424/133.1](#), [424/134.1](#), [424/184.1](#), [424/185.1](#),
[424/192.1](#), [424/193.1](#), [530/387.1](#), [530/387.3](#), [530/395](#)

CLAIMS:

What is claimed is:

1. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
2. The isolated polypeptide of claim 1, wherein x.sub.1 is 21.
3. A composition comprising: an isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21, and an agent selected from the group consisting of a therapeutic drug, a toxin, a radionuclide, a chromophore, a colorimetric molecule, and a fluorometric molecule, wherein the agent is linked to the polypeptide.
4. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the nucleotide sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1.
5. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
6. The fusion polypeptide of claim 5, wherein x.sub.1 is 21.
7. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

8. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transfected or transformed with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1,

under conditions such that the polypeptide is produced from the DNA.

9. The polypeptide of claim 8, wherein x.sub.1 is 157.

10. The polypeptide of claim 8, wherein x.sub.1 is 217.

11. The polypeptide of claim 8, wherein the method further comprises recovering the polypeptide.

12. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the sequence as set forth in SEQ ID NO:4; and (b) a polypeptide comprising the sequence from about x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

13. The isolated polypeptide of claim 12, wherein x.sub.1 is 21.

14. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the sequence from nucleotide x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73.

15. The isolated polypeptide of claim 14, wherein the DNA comprises the sequence as set forth in SEQ ID NO: 3.

16. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

17. The fusion protein of claim 16, wherein the fusion polypeptide comprises the sequence as set forth in SEQ ID NO:4 from amino acid 21 to amino acid 330.

18. The fusion polypeptide of claim 16, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

19. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transformed or transfected with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the nucleotide sequence x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73,

wherein the host cell is cultured under conditions such that the polypeptide is produced from the DNA.

20. The polypeptide of claim 19, wherein x.sub.2 is 13.

21. The polypeptide of claim 19, wherein x.sub.2 is 73.

22. The polypeptide of claim 19, wherein the method further comprises recovering the polypeptide.
23. A composition comprising a suitable carrier and a polypeptide of claim 1.
24. A composition comprising a suitable carrier and a polypeptide of claim 12.
25. A composition comprising a suitable carrier and a fusion polypeptide of claim 5.
26. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to X2 of SEQ ID NO: 2 having one amino acid deletion, insertion or substitution thereto, wherein x.sub.1 is 1 or 21 and x.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a sequence as set forth in SEQ ID NO: 20 or 22.
27. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to x.sub.2 of SEQ ID NO: 2 having a deletion of 1 to 5 terminally located amino acids, wherein x.sub.1 is 1 or 21 and X.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a

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L1: Entry 1 of 1

File: USPT

Jan 28, 2003

US-PAT-NO: 6512095

DOCUMENT-IDENTIFIER: US 6512095 B2

TITLE: Molecules designated B7L-1

DATE-ISSUED: January 28, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Baum; Peter R.	Seattle	WA		

US-CL-CURRENT: 530/350; 424/130.1, 424/133.1, 424/134.1, 424/184.1, 424/185.1,
424/192.1, 424/193.1, 530/387.1, 530/387.3, 530/395

CLAIMS:

What is claimed is:

1. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
2. The isolated polypeptide of claim 1, wherein x.sub.1 is 21.
3. A composition comprising: an isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21, and an agent selected from the group consisting of a therapeutic drug, a toxin, a radionuclide, a chromophore, a colorometric molecule, and a fluorometric molecule, wherein the agent is linked to the polypeptide.
4. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the nucleotide sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1.
5. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
6. The fusion polypeptide of claim 5, wherein x.sub.1 is 21.
7. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

8. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transfected or transformed with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1,

under conditions such that the polypeptide is produced from the DNA.

9. The polypeptide of claim 8, wherein x.sub.1 is 157.

10. The polypeptide of claim 8, wherein x.sub.1 is 217.

11. The polypeptide of claim 8, wherein the method further comprises recovering the polypeptide.

12. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the sequence as set forth in SEQ ID NO:4; and (b) a polypeptide comprising the sequence from about x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

13. The isolated polypeptide of claim 12, wherein x.sub.1 is 21.

14. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the sequence from nucleotide x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73.

15. The isolated polypeptide of claim 14, wherein the DNA comprises the sequence as set forth in SEQ ID NO: 3.

16. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

17. The fusion protein of claim 16, wherein the fusion polypeptide comprises the sequence as set forth in SEQ ID NO:4 from amino acid 21 to amino acid 330.

18. The fusion polypeptide of claim 16, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

19. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transformed or transfected with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the nucleotide sequence x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73,

wherein the host cell is cultured under conditions such that the polypeptide is produced from the DNA.

20. The polypeptide of claim 19, wherein x.sub.2 is 13.

21. The polypeptide of claim 19, wherein x.sub.2 is 73.

22. The polypeptide of claim 19, wherein the method further comprises recovering the polypeptide.
23. A composition comprising a suitable carrier and a polypeptide of claim 1.
24. A composition comprising a suitable carrier and a polypeptide of claim 12.
25. A composition comprising a suitable carrier and a fusion polypeptide of claim 5.
26. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to X2 of SEQ ID NO: 2 having one amino acid deletion, insertion or substitution thereto, wherein x.sub.1 is 1 or 21 and x.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a sequence as set forth in SEQ ID NO: 20 or 22.
27. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to x.sub.2 of SEQ ID NO: 2 having a deletion of 1 to 5 terminally located amino acids, wherein x.sub.1 is 1 or 21 and X.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a

Db 242 YPEVSVIS-GYDNNWYLQNEA-TLTCDAENPPTGYNNSTTMGTLPLPPFAVQAQALLI 299
 Qy 283 NNLAKTNDGTGYRCEASNTVGAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTITD 342
 Db 300 RPVDKPTNTLTCNVNAGARQELTVQVE-----GPPSEHS----- 338
 Qy 343 SRAGEETIGAVDHAVIGGVVAVVFMCLLIILGRYF 381
 Db 339 -----GMSRNAIFPLVLGILVF---LILLGIGIVF 365

RESULT 14
 neurotrophin - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: I56551
 R:Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
 J. Neurosci. 15, 2141-2156, 1995
 A:Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neu
 A:Reference number: I56551; MUID:95198094; PMID:7891157
 A:Accession: I56551
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-344 <RES>
 A:Cross-references: EMBL:U16845; NID:9755184; PIDN:AAAG7445.1; PID:9755185
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 10.5%; Score 231; DB 2; Length 344;
 Best Local Similarity 26.2%; Pred. No. 5.1e-09;
 Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

Qy 10 LLLLLLSAALIPTG-----DQGNLFTK---DVTWIEGEVATISQVNVKSDSDSVIQLNPN 62
 Db 14 LVVSLRLLELVPVTPGVRSGDAPPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN 70

Qy 63 RQTI-YFDFRPLKDSRQLLNFSSELKSLTNVVISDEGRYFCQLYTD-PPQESYTTI 120
 Db 71 RSTILYAGNDKWCLDPVYLLSNTQVSIQNVVYDEGPTCSVQTDNHPKTSRVHL 130

Qy 121 TVLPPRNLMIDIQDQAV-EGEIEVNTAMASKPATTIWFKNKELKKGSEVWSD 179
 Db 131 IVQVSPK--IVEISDSISINGNISLFCIA-TGRPEPTVTRHISPKAVGVSEDEYLE 187

Qy 180 MYTVTSQMLKLVH---KEDDGPVVICQVEHPAVTGNLTQRYLEVQYKPVQVHIQMTYPLQ 236
 Db 188 IQGITREQSGEVECSASNDVAAPVVRVN-----VTWVPPYIS-----EAK 229

Qy 237 GL-TREGDAFELTCEATGKPPQVMTVVRVDEMPQ-----HAVLSGNLFINNLM 286
 Db 230 GTGVFQKQKGLQCEASAVPS-ABFQFQKDKRLVEGKGVKVENRPFSLRLTFF--NVS 286

Qy 287 KTDNGTYRCEASNTVGAHSDYMLY 311
 Db 287 EHDYGNVTCVASNKLGHNTASIMLF 311

RESULT 15
 I38346
 elastic titin - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I38346
 R:Labelit, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330; PMID:7569978
 A:Accession: I38346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7962 <RES>
 A:Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
 C:Genetics:

A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q31

Query Match 10.4%; Score 228.5; DB 2; Length 7962;
 Best Local Similarity 26.1%; Pred. No. 4e-07;
 Matches 80; Conservative 55; Mismatches 130; Indels 41; Gaps 13;

Qy 35 TVIEGEVATISQVNVKSDSDSVIQ---LLN-----PNRQTIYFRDFRPLKDSRFQLLNPF 84
 Db 770 TVLDRDIAPFTKPLRNVDVSVNGTCLDCKIAGSLPMRVS-WFKDGKKEIAASDRYIAF 828

Qy 85 SSSELKVSLTNVVISDEGRYFCQLYTD-PPQESYTTITVLVPPRNLMIDIQDQAVEGEE 143
 Db 829 VEGTASLEIIRVDMNDAGNFTCRATNSVGSKDSSGALIVQEPFVTKPGSKD-VLPESA 887

Qy 144 IEVNTAMASKPATTIWFKNKELKG-----KSEVWSDMYTVTSQMLKVKHKEDD 196
 Db 888 VCLKSTFQGSTP-LTIRWFKGNKELVSGGSCYITKEALSSLELYLV-----KTS 937

Qy 197 GVPVICQVEHPAVTGNLTQRYLEVQYKPVQVHIQMTYPLQGLTREGDAFELTCEAIGK 256
 Db 938 SGTYTCKVSN--VAGGVECSANLEVK-EPATFVEKLEPSQ-LLKKGDTQLACKVTGTP- 992

Qy 257 PVMTVTVVRVDEMPQHA-----VLSGPNLFINNLTNDNGTYRCEASNTVGAHSDYML 310
 Db 993 PIKITWFANDREIKESKHRMSFVESTAVLRITDVGIEDSGEYVCEAQNAGSDHCSSIV 1052

Qy 311 VYVDDP 316
 Db 1053 IVKESP 1058

Search completed: May 27, 2004, 09:32:24
 Job time : 13.2283 secs

[illegible]

Db 62 SOLTWSRHGSGSMAVPHOTQGNYPSEKRLFEFAARLGTGLDASLRMFGRLVDEGNY 121
QY 105 FCOLYTDPPQESYTT---ITVLVPPRLMLDIQKOTAVEGEEIEV-NCTAMASKPATITR 160
Db 122 TC-LFVTFPQGSRSVDILWLVAKPN-TAEVQK-VOLTGKPPVAVRCVSTGGRPPAHIT 178
QY 161 WFKGNKELGKSEVEE-----WSDMYTIVTSQMLKVKHEDDGVFVICQVEHPAVTGNLQ 216
Db 179 W---HSDLGMPNTSQAPGLSGTIVTISLWILVPSQVDGKSVTKCKVEHSEPEKQLLT 235
QY 217 RYLEVQKQVHLOMTYPIQGLTRBGDAFELTCEAIKGPQPMVMTWVRVDDEMPQHAVLS 276
Db 236 VNLTVYTPPEVSIS-GYDNNWYLSQNEA-TLTCDAARSNPETGYNWSTTMGCLPPPPFAVAQ 293
QY 277 GPNLFINLNKNTDNGTVRCBASNIIVGKHSYMLVYVDRPTTIPPTTTTTTTTTTTT 336
Db 294 GAQLLRPVDKPIINTFICNVNVALGARQALTVQVKEGPPSPS----- 338
QY 337 LTIITDSRAGEEGTIGAVDHAVIGGVVAVVFMCLLILIGRYFARHKGT-----YFTH 392
Db 339 -----GMSNIIIFLILGIVI---LTLTGIGVYFYKRSRCSREFLWCHHL 380
QY 393 AKGADDAADATLAINAGQNNSEKKE 421
Db 381 SPSSEEHASA-----SANGYISYSDVSRE 404

RESULT 10

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Carcophthecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 234.5; DB 2; Length 392;
Best Local Similarity 24.4%; Pred. No. 3 4e-09;
Matches 100; Conservative 58; Mismatches 180; Indels 71; Gaps 16;

QY 1 AADPGLRLRLLLLLLAAALIPGQNLFTKQVTV--IEGEVATISC--QVNSKSDSVI 56
Db 8 AWPP-----LTLTLELSPPPTGDIIVQAPQVPGFLGDSVTLPCYLQVPMEEHV 61
QY 57 QLNPNR-----QTIYFRDRLKDSRFQNLNFSSELKYLTVNS-----ISDEGRY 104
Db 62 SOLTWSRHGSGSMAVPHOTQGNYPSEKRLFEFAARLGTGLDASLRMFGRLVDEGNY 121
QY 105 FCOLYTDPPQESYTT---ITVLVPPRLMLDIQKOTAVEGEEIEV-NCTAMASKPATITR 160
Db 122 TC-LFVTFPQGSRSVDILWLVAKPN-TAEVQK-VOLTGKPPVAVRCVSTGGRPPAHIT 178
QY 161 WFKGNKELGKSEVEE-----WSDMYTIVTSQMLKVKHEDDGVFVICQVEHPAVTGNLQ 216
Db 179 W---HSDLGMPNTSQAPGLSGTIVTISLWILVPSQVDGKSVTKCKVEHSEPEKQLLT 235
QY 217 RYLEVQKQVHLOMTYPIQGLTRBGDAFELTCEAIKGPQPMVMTWVRVDDEMPQHAVLS 276
Db 236 VNLTVYTPPEVSIS-GYDNNWYLSQNEA-TLTCDAARSNPETGYNWSTTMGCLPPPPFAVAQ 293
QY 277 GPNLFINLNKNTDNGTVRCBASNIIVGKHSYMLVYVDRPTTIPPTTTTTTTTTTTT 336
Db 294 GAQLLRPVDKPIINTFICNVNVALGARQALTVQVKEGPPSPS----- 338

QY 337 LTIITDSRAGEEGTIGAVDHAVIGGVVAVVFMCLLILIGRYFARHK 385
Db 339 -----GMSNIIIFLILGIVI---LTLTGIGVYFYRSR 369
RESULT 11
IXJNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:G214609; PIDN:AAA49909.1; PID:G214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo.
C;Comment: Several forms of NCAM are produced by alternative splicing.

C;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LI
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pre
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 1.3e-08;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 32 KDVTVEGEVATISC---QVNSK---DDSVIQLLN---PNQTIYFRDRLKDSRFQL 81
Db 199 KOIQVIVNVPPTIQARLQRLVATANNAESVLSVSCDADGFPDEISLWKKGEPIEDGE-EK 257
QY 82 LNPSSSELKSLTVNSISDEGRYFCOLYTDPPQESYTTITVLVPPRLMLDIQKOTAVEG 141
Db 258 ISFNEDQSESTIHHVKDEAEAYSC-IANNQAGEAEATLLKVAKPKITYVENKTAVEL 316
QY 142 EEIEVNTAMASKPATITRMFKNGE-----LACKSEVEESDMYTVTSQMLKXVHKE 194
Db 317 DEITLCEA-SGDIPISTWRTAVRNVISSEATTLGDHIVVKEHRM---SANTLKDIOY 371
QY 195 DGGVPVICQVEHPAVTGNLQRYLEVYKQPVHIOQMTYPLQGLTRBGDAFELTCEAIGK 254
Db 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQAPKIR---GPVVVYTWEGPNVITCEVFAH 425
QY 255 PQVMVMTWVRVDDEMPQH-----AVLSGP---NLFINLNKNTDNGTVRCBASNIIVGKHS 306
Db 426 PR-AAVTFRFDGQLLPSSNFSNFKIYSGPTSSSLEVPDSEDFGNVCTAINTIGHEPS 484
QY 307 DYMLVYVDRPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
Db 485 EFILVQADTFSS---FAIRKVEPYSTVMIVFDEPDSTGG 521

```
QY 329 TTTTTLTILTIITDSRAGEGTIGAVDHAVIGGVAVVV 367
Db 344 -----AGAGATGG-----IIGGIIIAII 361

RESULT 7
I68093
P:276-331/Domain: immunoglobulin homology <IMM>
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C/Accession: I68093
R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A/Title: The human PR2 gene, related to the human poliovirus receptor gene (PVR), is th
A/Reference number: I53960; MUID:95347610; PMID:7622062
A/Accession: I68093
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-538 <RES>
A/Cross-references: GB:S79172; NID:G1042204; PID:G1042205
C/Genetics:
A/Gene: PR2delta
C/Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 238.5; DB 2; Length 538;
Best Local Similarity 22.8%; Pred. No. 2.6e-09;
Matches 110; Conservative 63; Mismatches 196; Indels 113; Gaps 17;

QY 2 APPGLRLRLLLLSAALIPITGQMLFTKQVTVIEGEVATISCQVKNKSDSVIQLNP 61
Db 12 SPPTPLLPILLLL-----LLETG-AQDVRVQVLPVRG-----QLGGVELPCHLLPP 59
QY 62 -----NRQTIYFRDPRPKDSR-----QLNFSSS----- 87
Db 60 VPGLYISLVTWQRPDAPANQNV--AAFHPKMGSPFSPKPSRSLFSVSAKQSTGQTE 117
QY 88 ----ELKVSILTNVSIISDEGRYFCOLYTDPP--POESYTTITVLVPPRLMIDIQDRTAVEG 141
Db 118 AELQDATLALHGLTVEDEGNVTCBFATPKGSRGVTWLRVIAKPKN-QAEAKQVTSQD 176
QY 142 EEIENVCTAMASKPATIRWPKG-NKELKGKSEVEWSDMYTTSQMLKLVKHEDDGVV 200
Db 177 PTTVALCISKEGRPPARISLWSSLDWEAKETQVSGTLAGTVITVTSRFTLVPSGRADGVTV 236
QY 201 ICQVEHPAVTNLQTRYLEYQKPVQHIQMTYPLQGLTREGDAFELTCEAIGKPPQVMV 260
Db 237 TCKVEHSEFEPALIPVTLVRYPEVISIS-GYDDNWYLGRTDA-TLSCDVRSNPEPTGY 294
QY 261 TWVRVDDMPQHAVLSGNLFINLNKTDNGTYRCEASNIYKRAHSDMYLYVYDPTTIP 320
Db 295 DWSITSGFTFTSAVAQGSQVIAHVSLENTFVCTVTNAVGMGRAEQVIVRETPTNT-- 352
QY 321 PPTTTTTTTTTTILTIILDSRAGEGTIGADVHVGAVVAVVFMCLLIILGRY 380
Db 353 -----AGATGG-----IIGGIIIAITATAVAATGILICR 383
QY 381 PARHKGTYFTHEAKGADDAAD-----TALINAE-----GGQNNSEKKE 421
Db 384 QORKEQT-----LQAEDEDELEGPPSKPTPKAKLEAQEMPQSLFTLGASERSPLKTP 438
QY 422 YF 423
Db 439 YF 440

RESULT 8
JE0099
neural cell adhesion molecule 1 - African clawed frog
N/Alternate names: N-CAM 1
C/Species: Xenopus laevis (African clawed frog)
C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: JE0099
R/Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A/Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A/Reference number: JE0099; MUID:98204770; PMID:9535795
A/Accession: JE0099
A/Molecule type: mRNA
A/Residues: 1-725 <KUD>
A/Cross-references: DDBJ:AB008162; NID:G3116226; PIDN:BAA25931.1; PID:G3116227
A/Experimental source: heart
C/Comment: This protein mediates and regulates various cell-cell interactions through bo
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.8%; Score 238; DB 2; Length 725;
Best Local Similarity 26.2%; Pred. No. 4.2e-09;
Matches 89; Conservative 61; Mismatches 148; Indels 42; Gaps 15;

QY 32 KQVTVIEGEVATISC---QVN---KSDSVIQLLN---PNRQTIYFRDPRPKDSRFQL 81
Db 159 KDIQVIVNVPPTIQARQLRVNATAKMAESVLSVSCDADGFPDPEISWLKKGEPEDGE-EK 257
QY 82 LNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTITVLVPPRLMIDIQDRTAVEG 141
Db 258 ISFNEQDSEMTIHVKEKDDAEAYSC-IANNQAGEAEATILLYAKPKITYVENKTAVEL 316
QY 142 EEIENVCTAMASKPATIRWPKGKE-----LKGKSEVEWSDMYTTSQMLKLVHKE 194
Db 317 DEITLCEA-SGDPISITWRTAVRNISSEATLDGHIVVKEHRM-----SALTLDIQY 371
QY 195 DGGVPVICQVEHPAVTNLQTRYLEYQKPVQHIQMTYPLQGLTREGDAFELTCEAIGK 254
Db 372 TDAGEYFCIASNE-IGVDMQAM-YFEVQYAPKIR---GTVVYTWEGNPVNITCEVFAH 425
QY 255 PQVMVTVWRVDDMPQH-----AVLSGP---NLFINNLTNGTYRCEASNIYKRAHS 306
Db 426 PR-AAVTFRDGGLPSSNFNISKIYSGPTSSSLEVPDSEDFGNYNCTAINTIGHS 484
QY 307 DYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTITLITDSRAG 346
Db 485 EFTLVQADTFSS---FAIRKVEPYSSTVIMVFEDEPSTGG 521

RESULT 9
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: A44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: A44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-417 <KOI>
A/Cross-references: GB:S48777
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 237; DB 2; Length 417;
Best Local Similarity 23.8%; Pred. No. 2.4e-09;
Matches 107; Conservative 68; Mismatches 194; Indels 80; Gaps 18;

QY 1 AAPGLRLRLLLLSAALIPITGQMLFTKQVTV--IEGEVATISC--QVKNKSDSVI 56
Db 8 AWPP-----LLLTLLLSWPPPTGDIIVQAPQVPGFLGDSVTLPCYLQVPGMEETHV 61
QY 57 QLQNPENR-----QTIYFRDPRPKDSRFQLNFSSELKVSILTNV-----ISDEGRY 104
```


F:375-467/Domain: intracellular #status predicted <INT>
F:54-131,174-229,274-320/disulfide bonds: #status predicted
F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 246.5; DB 1; Length 467;
Best Local Similarity 21.6%; Pred. No. 68-10;
Matches 101; Conservative 72; Mismatches 196; Indels 99; Gaps 16;

QY 4 PGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEV---ATISQV-----48
Db 14 PTLPLPLLLLL---LQETG-AQDVVRVRLPEVRGLGTGTPCHLPPITERVSQVT 68
QY 49 -NKSDSVTLQNLNPNQTIYFRDPLKDSRQL-----LNFSSSELKVSILTNVIS 99
Db 69 WORLDGTVAFAHPS---FGVDFPNSQFSKORLSFVRARPETNADRLDATLAFLRGLRVE 124
QY 100 DSGRYFCOLYTOP--POESYTTITVLVPRNLMDIQKDTAVEGEIEV-----NCT 149
Db 125 DGNVTCFATPENGTRGRVTLRLVIAQEN-----HAEAQEVITIGPQSVAVARCV 175
QY 150 AMASKPATTIRWPKG-NKELKGKSEVEEWSMDYTVTSQMLKVKHEDDGVPIQVHEPA 208
Db 176 STGGRRPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKTCRVEHES 235
QY 209 VTGNLQORYLEVOYKPVQVHIQNTYPLQGLTREGDAFELTCEALGKPOPMVMTWVRVDDE 268
Db 236 FEBPILLPVTLSVRYPEVVIS-GYDDNMYLGRSEAI-LTCDVRSNPETDYMSTTSVG 293
QY 269 MPQHAVLSGNLFINNLKNTDNGTYRCEASNIYGVKASDMLVYVDPPTTIPPTTTTTT 328
Db 294 FPASAVAQSSQLLVHSDVRMWNFTTCTATNAVGTGRAQVILVRTPQA-----343
QY 329 TTTTTLTIITIDSRAGEEGTIGAVDHAVIGGVAVVFA--MLCLLIILGRYFAHK 386
Db 344 -----SR-----DVGPLVWAGVGTTLLVLLAGFLAILLLRGRRRKSPG 384
QY 387 TYPTHEAKGADDA-----ADADTAIINAEAGGONNSEEKKE 421
Db 385 GGGNDGRGSDYDKPTQVFGNGGVFWRASAPPEMRPDGREEDDEEEEEE 432

RESULT 5
JC4024
poliovirus receptor-related protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C:Accession: JC4024
R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, C.; Dubre
Gene 155, 261-265, 1995
A:Title: Complementary DNA characterization and chromosomal localization of a human gene
A:Reference number: JC4024; MUID:95237621; PMID:7721102
A:Accession: JC4024
A:Molecule type: mRNA
A:Residues: 1-518 <LOP>
A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C:Genetics:
A:Gene: GDB:PVRR1
A:Cross-references: GDB:583951
A:Map position: 11q23-11q24
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F:356-379/Domain: transmembrane #status predicted <TM>
F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.1%; Score 243; DB 2; Length 530;
Best Local Similarity 22.6%; Pred. No. 1-2e-09;
Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;

QY 4 PGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEV---ATISQV-----48
Db 14 PTLPLPLLLLL---LQETG-AQDVVRVRLPEVRGLGTGTPCHLPPITERVSQVT 68
QY 49 -NKSDSVTLQNLNPNQTIYFRDPLKDSRQL-----LNFSSSELKVSILTNVIS 99
Db 69 WORLDGTVAFAHPS---FGVDFPNSQFSKORLSFVRARPETNADRLDATLAFLRGLRVE 124
QY 100 DSGRYFCOLYTOP--POESYTTITVLVPRNLMDIQKDTAVEGEIEV-----NCT 149
Db 125 DGNVTCFATPENGTRGRVTLRLVIAQEN-----HAEAQEVITIGPQSVAVARCV 175
QY 150 AMASKPATTIRWPKG-NKELKGKSEVEEWSMDYTVTSQMLKVKHEDDGVPIQVHEPA 208
Db 176 STGGRRPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKTCRVEHES 235
QY 209 VTGNLQORYLEVOYKPVQVHIQNTYPLQGLTREGDAFELTCEALGKPOPMVMTWVRVDDE 268
Db 236 FEBPILLPVTLSVRYPEVVIS-GYDDNMYLGRSEAI-LTCDVRSNPETDYMSTTSVG 293
QY 269 MPQHAVLSGNLFINNLKNTDNGTYRCEASNIYGVKASDMLVYVDPPTTIPPTTTTTT 328
Db 294 FPASAVAQSSQLLVHSDVRMWNFTTCTATNAVGTGRAQVILVRTPQA-----343

QY 114 QBSYTTITVLVPRNLMDIQKDTAVEGEIEV---NCTAMASKPATTIRWFKGNKEIK 169
Db 134 RESQNLNLTWAKKPTTWIEGTQAVLRKAKGQDDKVLVATCTSANGKPPSVSW---ETRLK 190
QY 170 GKSEV--EWSDM--YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQORY-----LE 220
Db 191 GEARVPGSGTGPMAVTVISRYRLVPSREAHQOSLACIV-----NYHMDRFKSLTLN 243
QY 221 VOYKPOVHIQ---MTYPLQGLTREGDAFELTCEALGKPOPMVMTWVRVDDEMPQHAVLSG 277
Db 244 VOYEDEVITIEGFGNWLQRM-----VKLTCKADANPATEYHHTYTLNGLSPKGEAQN 298
QY 273 PNLFINN-LNKTDNGTYRCEASNIYGVKASDMLVYVDPPTTIPPTTTTTTTTTT 336
Db 299 RTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITFPYTPSP-----344
QY 337 LTIITDSRAGEEGTIGAVDHAVIGGVAVVFA--MLCLLIILGRYFA---RH--KGTYF 389
Db 345 -----EHRRAGPVPTAIIGSVAGSI---LLVLIVGGI VVALRRRHHRTFKGDYS 391
QY 390 T-----HEAKGA-----DDAADADTAIINAEAGGONNSEEKKE 421
Db 392 TKKHVYGVNGSKAGIPQHHPMAQNLOYPDDSDDEKKA--GPLGGSSYEHEEE 443

RESULT 6
A53437
poliovirus receptor mpvr - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with
A:Reference number: A53437; MUID:94179228; PMID:8132569
A:Accession: A53437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <AOK>
A:Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A:Experimental source: C57/BL6, brain
A:Note: Sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 11.1%; Score 243; DB 2; Length 530;
Best Local Similarity 22.6%; Pred. No. 1-2e-09;
Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;

QY 4 PGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEV---ATISQV-----48
Db 14 PTLPLPLLLLL---LQETG-AQDVVRVRLPEVRGLGTGTPCHLPPITERVSQVT 68
QY 49 -NKSDSVTLQNLNPNQTIYFRDPLKDSRQL-----LNFSSSELKVSILTNVIS 99
Db 69 WORLDGTVAFAHPS---FGVDFPNSQFSKORLSFVRARPETNADRLDATLAFLRGLRVE 124
QY 100 DSGRYFCOLYTOP--POESYTTITVLVPRNLMDIQKDTAVEGEIEV-----NCT 149
Db 125 DGNVTCFATPENGTRGRVTLRLVIAQEN-----HAEAQEVITIGPQSVAVARCV 175
QY 150 AMASKPATTIRWPKG-NKELKGKSEVEEWSMDYTVTSQMLKVKHEDDGVPIQVHEPA 208
Db 176 STGGRRPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKTCRVEHES 235
QY 209 VTGNLQORYLEVOYKPVQVHIQNTYPLQGLTREGDAFELTCEALGKPOPMVMTWVRVDDE 268
Db 236 FEBPILLPVTLSVRYPEVVIS-GYDDNMYLGRSEAI-LTCDVRSNPETDYMSTTSVG 293
QY 269 MPQHAVLSGNLFINNLKNTDNGTYRCEASNIYGVKASDMLVYVDPPTTIPPTTTTTT 328
Db 294 FPASAVAQSSQLLVHSDVRMWNFTTCTATNAVGTGRAQVILVRTPQA-----343

R; Sulston, J.
submitted to the EMBL Data Library, December 1994
A; Reference number: Z19355
A; Accession: T20992
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-5175 <WIL>
A; Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A; Experimental source: clone F15G9
R; Kershaw, J.
submitted to the EMBL Data Library, June 1998
A; Description: Hemiscitin is required for hemidesmosome mediated cell adhesion and germ-
A; Reference number: Z22396
A; Accession: T43290
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-5198 <VOG>
A; Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R; Sulston, J.
submitted to the EMBL Data Library, December 1994
A; Reference number: Z19355
A; Accession: T20993

Query Match 11.9%; Score 261.5; DB 2; Length 5175;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;

QY 34 VTVEGEVATISQVANKSDSDSVIQLNPNRQTIYFRDRL-----KDSRFQLNFSSEL 89
Db 2200 VTAIKGALPFKPID-DDK-----NFKGQIWLRYNPIDLEAEDARITRL---SNDR 2249
QY 90 KVSILTVNSISDEGRYFCQLYDPPQSYT-TITVLVPPRLMIDIOKD-TAVEGEEIEVN 147
Db 2250 RLITLNVTEDEGQYSCRKNDAGENSDFKATVLVPTTIIMLDKDKNTAVEHSTVLS 2309
QY 148 CTAMASKPATIIRWFKG-----NKLKGKSEVEWSDMYTTSQMLKLVHK 193
Db 2310 CPA-TGKPEPDIWFKDGEAHIENIADIIPNGELNG-----NQLKITRIK 2354
QY 194 EDGVPVICQVEHPAVTGNLQYLYEVQYKPOVH---IQMTYPLQGLTREGDAFELTCE 250
Db 2355 EGDAGKYTCBADNSA--GSVEQDVNVNVTIPIKEDGIPSDYESQ---QNERVVISCP 2408
QY 251 AIGKPPQVMVTVRVDDMPQHAVL-----SGPNLFINNKNKTNGTYRCASINIVGKAHS 306
Db 2409 VYARP-PAKITWLKAGPLQSDKFKVTSANGOKLYLFKLRETDSKTYCTIATNEAGTDKR 2467
QY 307 DYMLVYVDPPTTIPP-----PTTTTTTTTTTTTTTTTTTTTTITITDSRAGE 347
Db 2468 DFKVSMVLVAFSDFEPNIVRRITVNSGNPSTLHCPAKGSPSPITWLKDGNAIE 2520

RESULT 3
T43290
hemiscitin precursor - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 18-Feb-2000
A; Accession: T43290; T20993; T24734
R; Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A; Reference number: Z22396
A; Accession: T43290
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-5198 <VOG>
A; Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R; Sulston, J.
submitted to the EMBL Data Library, December 1994
A; Reference number: Z19355
A; Accession: T20993

A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-5198 <WIL>
A; Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A; Experimental source: clone F15G9
R; Kershaw, J.
submitted to the EMBL Data Library, December 1994
A; Reference number: Z19929
A; Accession: T24734
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-5198 <W12>
A; Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A; Experimental source: clone T09B9
C; Genetics:
A; Gene: him-4; F15G9.4b
A; Map position: X
A; Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A; 2512/2; 2593/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
A; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;
Query Match 11.9%; Score 261.5; DB 2; Length 5198;
Best Local Similarity 24.8%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;

QY 34 VTVEGEVATISQVANKSDSDSVIQLNPNRQTIYFRDRL-----KDSRFQLNFSSEL 89
Db 2200 VTAIKGALPFKPID-DDK-----NFKGQIWLRYNPIDLEAEDARITRL---SNDR 2249
QY 90 KVSILTVNSISDEGRYFCQLYDPPQSYT-TITVLVPPRLMIDIOKD-TAVEGEEIEVN 147
Db 2250 RLITLNVTEDEGQYSCRKNDAGENSDFKATVLVPTTIIMLDKDKNTAVEHSTVLS 2309
QY 148 CTAMASKPATIIRWFKG-----NKLKGKSEVEWSDMYTTSQMLKLVHK 193
Db 2310 CPA-TGKPEPDIWFKDGEAHIENIADIIPNGELNG-----NQLKITRIK 2354
QY 194 EDGVPVICQVEHPAVTGNLQYLYEVQYKPOVH---IQMTYPLQGLTREGDAFELTCE 250
Db 2355 EGDAGKYTCBADNSA--GSVEQDVNVNVTIPIKEDGIPSDYESQ---QNERVVISCP 2408
QY 251 AIGKPPQVMVTVRVDDMPQHAVL-----SGPNLFINNKNKTNGTYRCASINIVGKAHS 306
Db 2409 VYARP-PAKITWLKAGPLQSDKFKVTSANGOKLYLFKLRETDSKTYCTIATNEAGTDKR 2467
QY 307 DYMLVYVDPPTTIPP-----PTTTTTTTTTTTTTTTTTTTTTITITDSRAGE 347
Db 2468 DFKVSMVLVAFSDFEPNIVRRITVNSGNPSTLHCPAKGSPSPITWLKDGNAIE 2520

RESULT 4
HLMSP3
poliovirus receptor homolog precursor - mouse
C; Species: Mus musculus domesticus (western European house mouse)
C; Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 22-Jun-1999
R; Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A; Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A; Reference number: A38211; MUID:92219365; PMID:1560525
A; Accession: A38211
A; Molecule type: DNA
A; Residues: 1-467 <MOR>
A; Cross-references: GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C; Superfamily: poliovirus receptor; immunoglobulin homology
C; Keywords: duplication; glycoprotein; transmembrane protein
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F; 26-354/Domain: extracellular #status predicted <EXT>
F; 47-133/Domain: immunoglobulin homology <IMM>
F; 167-231/Domain: immunoglobulin homology <IMM2>
F; 267-322/Domain: immunoglobulin homology <IMM3>
F; 355-374/Domain: transmembrane #status predicted <TMN>

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.283 Seconds

(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLLLLSAAL.....TAINAEGGNNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	270	12.3	407	T08732	hypothetical prote
2	261.5	11.9	5175	T20992	hypothetical prote
3	261.5	11.9	5198	T43290	hemikentlin precurs
4	246.5	11.2	467	HLMP3	poliovirus recepto
5	244	11.1	518	JC4024	poliovirus recepto
6	243	11.1	530	A53437	poliovirus recepto
7	238.5	10.9	538	T168093	poliovirus recepto
8	238	10.8	725	JE0099	PRR2 delta - human
9	237	10.8	417	A44194	poliovirus recepto
10	234.5	10.7	392	B44194	poliovirus recepto
11	234	10.7	1088	IJXLNL	neural cell adhesi
12	232.5	10.6	392	1 RWHUPD	poliovirus recepto
13	232.5	10.6	417	1 RWHUPD	poliovirus recepto
14	231	10.5	344	T156551	neurotrophin - rat
15	228.5	10.4	7962	I38346	elastic titin - hu
16	226	10.3	4162	T42633	connectin/titin -
17	225	10.2	1011	T13669	connectin/titin -
18	222	10.1	725	JE0100	neurotrophin - fr
19	222	10.1	1092	1 JN0635	neural cell adhesi
20	220.5	10.0	338	JC5519	50K glycoprotein p
21	220	10.0	478	I53960	PRR2 alpha - human
22	217.5	9.9	345	S03199	opioid-binding pro
23	215.5	9.8	345	JC4025	opioid-binding cel
24	215.5	9.8	588	A45254	surface glycoprote
25	214	9.7	588	JH0506	adhesion molecule
26	212	9.6	4391	T A38096	perlecan precursor
27	210.5	9.6	812	B42632	cell adhesion mole
28	210.5	9.6	932	A42632	cell adhesion mole
29	209.5	9.5	345	JC1239	opioid-binding pro

30	209.5	9.5	584	2	I50419	s-glycerin precurs
31	207.5	9.4	646	2	I38049	cell surface glyco
32	206.5	9.4	338	2	JC4776	limbic-system-asso
33	206.5	9.4	862	2	I49583	differentiation an
34	206.5	9.4	868	2	A48512	CD22 homolog/B lym
35	206	9.4	847	2	JH0371	B-cell adhesion pr
36	204	9.3	702	2	A36319	carcinoembryonic a
37	203.5	9.3	583	2	I39428	alcam - human
38	202	9.2	1443	2	I50600	neogenin - chicken
39	200.5	9.1	338	2	JC1238	opioid-binding pro
40	200.5	9.1	765	2	C42632	cell adhesion mole
41	200	9.1	587	2	JH0464	DM-GRASP precursor
42	197	9.0	3707	2	S18252	heparan sulfate pr
43	196.5	8.9	1241	2	T37190	nephrin - human
44	195	8.9	1323	2	PN0568	connectin 3B - chi
45	193	8.8	761	1	IJHUNG	neural cell adhesi

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFP566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C;Accession: T08732

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16474

A;Accession: T08732

A;Molecule type: mRNA

A;Residues: 1-407 <OTT>

A;Cross-references: EMBL:AL050071

A;Experimental source: fetal kidney; clone DKFP566B0846

C;Genetics:

A;Note: DKFP566B0846.1

Query Match 12.3%; Score 270; DB 2; Length 407;

Best Local Similarity 27.0%; Pred. No. 1.1e-11;

Matches 85; Conservative 58; Mismatches 124; Indels 48; Gaps 13;

Qy	1C2	GRYFCOLYTD--PQESYTTITVLVPPRLMIDIQDXTAVEG--EIEVNCTAMASKPAT 157
Db	2	GKVICKAVTFPLGNAQSSTTVLVEPTVSLIK-GPDSLIDGNETVAAICIAATGKPA 60
Qy	158	TIRWFKGNKELGKSEVEWSDMY-----TVTSQMLKVHKEDDGVVICOVHSPAVTGN 212
Db	61	HIDW-EGD-----LGEMSTTTSFPNETATISQYKLFPTFRFARGRRITCVVHKPALEKD 114
Qy	213	LOTQRYLEVQYKPVHIQMTYPLQGLTREGDAPELTCFAIGKQPVMVTVVRVDEMPQH 272
Db	115	IRYSFILDIQAYPEVSVTGDGNWFVGRKG--VNLACNADANPPPKSVWSRLDGQWPDG 172
Qy	273	AVLUSGNL-FINNINKDNGTRCEASNIVGKAHSYMLVYVDDP--TTIPP-----PTT 324
Db	173	LLASDNLHFVHPLTENYSGVICKVTNSIGQRSDQKVIYISDPPTTTTIQPTIQWHPST 232
Qy	325	TTTTTTTT-----TTTILTIITSRAGEEGTICAVDHAIVGGVAVVVFAMLCILI- 375
Db	233	ADIEDLATEPKLPPFLPLTLATI-----KODTIATIASVVGVALFVLVSLAGIFC 285
Qy	376	-----ILGRYFARH 384
Db	286	YRERRTRFGDYFAKN 300

RESULT 2

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

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QY 279 TWVRVDEMQHVAISGNLFINNANKTDNGTYRCEASIVGKAHSDYMLYVDDPTTIP 338
Db 300 LWEK-EGSVPLKWTQESALIFPLNKS DSGTYGCTATSNWGSYKAYTTLNVNDPS---P 355
QY 339 PPTTTTITTTTTTITLTITDTSRAGEBSIRAVDHAVIGGVAVVVFAMLCLLIILGRY 398
Db 356 VPSSSTY-----HAIIGGIVAFIVFLLIIMLIFLGHY 388
QY 399 FARHKGTYFTHAKGADADADATAIINARGGNNSEKKEYFI 442
Db 389 LIRHKGTYLTHAKGSDADADATAIINARGGSGDDKKEYFI 432

RESULT 15
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-05
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
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; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
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; EARLIER APPLICATION NUMBER: 60/048,974
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; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 947
; LENGTH: 227
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-205-258-947

Query Match 14.7%; Score 335; DB 4; Length 227;
Best Local Similarity 33.8%; Pred.No.1.6e-21;
Matches 78; Conservative 48; Mismatches 97; Indels 8; Gaps 5;

QY 106 ELKVSILNVSISDEGRYFCQLYTDPPQESYTTITVLVPPNLMIDIQDXTAVEGEIEVN 165
Db 1 ELSISISNALADEGEYTCISITMPVPTAKSLVTLVIGIPQKPIITGYKSSLREKDTATLN 60
QY 166 CTAMASKPATTTTWFKGNTELKKG-SEVEEWS--MYVTSQLMLKVHKEDDGVVICQV 222
Db 61 COSSGSKPAARLTWRKGDQLHGEPTRIQEDPNKGKFTTVSSSVTFQVTRDDGASIVCSV 120
QY 223 ERPAVTG-NLQQRVLEVOYKQVHIQMTYPLQGLTREGDALELTCEATGKPPVMTWV 281
Db 121 NHESLKGADRSQSRIEVLVYTTAMIRPDPP--HPREGQKLLHCEGRNFPVPOQYLWE 177
QY 282 RVDDEMPQHAVLGSNPLFINNKNKTDNGTYRCEASIVGKAHSDYMLYVDD 332
Db 178 K-EGSVPLKWTQESALIFPLNKS DSGTYGCTATSNWGSYKAYTTLNVND 227
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Search completed: May 27, 2004, 09:36:56
Job time : 17.1676 secs

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mathier, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902/775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLLLLFSAALIPGTG-----DQNLFTKDVTVIEGEVATISCOVNKSDSDSVIQL 76
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDQSQWTSDETVAAGTVLKCQVKDHDSDSLQW 62
Qy 77 LNPNRQTIYFRDPLKDSRFLQNLNFSSELKSLTNVSIISDEGRYFCQLYTDPDPQESYT 136
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Db 63 SNPAQQTLYFGEKRALRDNRNLIQVLTSTPHLSISISNVALADEGEYTCSTFTVPRVAKS 122
Qy 137 TITVLVPPRLNLMIDIOKDTAVEGEEIEVNCVTAMASKEPATTIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQPIITGYKSSREKDTATINCQSGSKPAARLTWRKQGEUHGEPRIQED 182
Qy 196 SD--MYTTSQMLMKVHKEDDGVFVQCQHPAVTG-NLQOTRYLEYQYKPOVHIQMTYP 252
Db 183 PNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGAADRSTQRIEVLVYPTAMIRDPDP 242
Qy 253 LQGLTREGDALEITCEALGKQPQVWTVWVRVDEMPQHAVLSGPNLFINNLTNDGTYR 312
Db 243 ---HPREGQKLLHCEGRGNPFQQYLWER-EGSVPLPKMTQESALIFPFLINKSDSGTYG 298
Qy 313 CEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTITSDRAGEGSRV 372
Db 299 CTATSNMGSKAYTLNVNDFS---PVPSSSYV----- 329
Qy 373 DHAIVGGVAVVVFVAMLCIIILGRYPARHKGYFTTHEAKGADDAADADTAIINAEGQN 432
Db 330 -HAIGGIVAFIVFLLIIMLIFLGHVLRHKGYLTHEAKGSDDADPADTAIINAEGQS 388
Qy 433 NSEKKEYFI 442
Db 389 GGDDKKEYFI 398

RESULT 14
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match      31.6%; Score 722; DB 4; Length 432;
Best Local Similarity 36.4%; Pred. No. 4.9e-55;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

Qy 22 PGLRLRLLLLFSAALIPGTG-----DG-----QNL----- 47
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDQSQWQOELEGLTAPLDEAISTVWSSPDMLAS 62
Qy 48 -----FTKDVTVIEGEVATISCOVNKSDSDSVIQLNPNRQTIYFRDPLKDSRFLQNL 102
Db 63 QDSQWTSDETVAAGTVLKCQVKDHDSDSLQWSNPAQOTLYFGEKEALRDNRIQLVTS 122
Qy 103 SSSELKSLTNVSIISDEGRYFCQLYTDPPOESYTTITVLVPPRLNLMIDIOKDTAVEGEEI 162
Db 123 TPHELSSISNVALADEGEYTCSTFTVPRVAKSLVTLGIPQPIITGYKSSLRKDTA 182
Qy 163 EVNTAMASKEPATTIRWFKGNTELKKG-SEVEWSD--MYTTSQMLMKVHKEDDGVVPI 219
Db 183 TLNCQSGSKPAARLTWRKQGEUHGEPRIQEDNGKTFVSSSVTFQVTRDDGASIV 242
Qy 220 COVEHPAVTG-NLQOTRYLEYQYKPOVHIQMTYFLOGLTREGDALEITCEALGKQPQVW 278
Db 243 CSVNHESLKGAADRSTQRIEVLVYPTAMIRDPDP---HPREGQKLLHCEGRGNPFVQY 299
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; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-778-510-6

Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLLLLFSAALIPGT-----DQNLFTKDVTVIEGEVATISQVKNKSDSVIQL 76
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDDSQPWTSDETVAGTVVLKQVKDHEDSSLQW 62
Qy 77 LNPNQTIYFRDFRPLKDSRFQLNFSSELKSVLTNVSISDEGRYFCQLYTDPQESYT 136
Db 63 SNPAQQTLYFGKRALDRNRQLVTSSTPHELSISISNVALADGEYTCISFTMPVRTAKS 122
Qy 137 TITVLVPPRNLMDIQDITAVEGEEIEVNCNTAMASKPATTIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKQDELHGFETRIQED 182
Qy 196 SD--MYVTSQLMLKVHEDGVPVICQVEHPAVTG-NLQTXYLEVQYKQVHIQMTYP 252
Db 183 PNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRILEVLYTPTMIRPDPP 242
Qy 253 LQGLTREGDALEICEATGKQPQVWTVWRVDDDEMPQHAVLSGNLFINNLTNDNGTYR 312
Db 243 ---HPREQKULLHCEGNGNVPQOYLMEK-EGSVPLPKMTQESALIPFPPLNKSDSGTYG 298
Qy 313 CEASNIVGKAHSDVYLYVDPPTTIPPTTTTPTTTTPTTTTITITITDSRAGEGSIKAV 372
Db 299 CTATSNMGSYKAYTLNVNDS---PVSSSTY----- 329
Qy 373 DHAIVGGVAVVVFAMLCILLIRYFARHKGTYFTHEAKGADDAADATTAIINAEQQN 432
Db 330 -HAIGGIVAFIVFILLIMLIFLGHYLRHKGTYLTHEAKGSDDAPADATTAIINAEQQS 388
Qy 433 NSEKKEYFI 442
Db 389 GGDDKKEYFI 398

RESULT 11
US-09-778-794A-84
; Sequence 84, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-794A-84

Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLLLLFSAALIPGT-----DQNLFTKDVTVIEGEVATISQVKNKSDSVIQL 76
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDDSQPWTSDETVAGTVVLKQVKDHEDSSLQW 62
Qy 77 LNPNQTIYFRDFRPLKDSRFQLNFSSELKSVLTNVSISDEGRYFCQLYTDPQESYT 136
Db 63 SNPAQQTLYFGKRALDRNRQLVTSSTPHELSISISNVALADGEYTCISFTMPVRTAKS 122
Qy 137 TITVLVPPRNLMDIQDITAVEGEEIEVNCNTAMASKPATTIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKQDELHGFETRIQED 182
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Db 363 VVFTLCSIFLLGRYLARHKGYTLTNEAKGAEDAPDADTAIINAEGSQVNAEKKEYFI 421

RESULT 8

US-08-660-531-1

; Sequence 1, Application US/08660531

; Patent No. 6221845

; GENERAL INFORMATION:

; APPLICANT: Chrysler, Susanna M.S.

; APPLICANT: Sinha, Sukanto

; APPLICANT: Keim, Pamela S.

; APPLICANT: Anderson, John P.

; TITLE OF INVENTION: Beta-Secretase

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,531

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/480,498

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15270-002210US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 421 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-660-531-1

Query Match 39.2%; Score 895.5; DB 3; Length 421;

Best Local Similarity 45.1%; Pred. No. 2.9e-70;

Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 44 GQLFTKDVTVIEGAVATISQVKNKSDSVTLQNLNPNRTIYFDRPLKDSRFQLNFS 103

Db 10 GQPLTONVTVIEGTAILECRVDQNTSLQSNPAQQTLYFDKKALRDNRILVRAS 69

QY 104 SSELKVSILTNVISDEGRYFCQLYTDPQESYTTITVLVPPRNLMIDIQDVAEGEEIE 163

Db 70 WHELISVSDVSLSDSQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSPVMEGLMQ 129

QY 164 VNCETAMASKATTIRWPKGNTELKGEVEWES---DMYVTSQMLKVKHKEDDGVVVIC 220

Db 130 LTCKTSGSKPAADIRWPKNDKEIKDVLYLKEEDANRKTFTVSSLDPRVDRSDGVAVIC 189

QY 221 QVEHPAVTGNLQ-TQRYLEVQYKQVHIQMTYPLQGLTRGDALCEALGKQPVMVT 279

Db 190 RVDESLNATPQAVAMQVLEIHTYTSVKI---IPSTPPEQGPILLICSGKGPLPEPVL 246

QY 280 WVRVDDM--PQHAVLSGPNLFINNKNKTNGTYRCEASNIYVKAHSDYMLVYVDPPTTI 337

Db 247 WTKDGGELPDRVMVSGREINILFLNKTNGTYRCEATNTIGQSSAEYVLIVHDVNTL 306

QY 338 PPPTTTTTTTTTTTTTTTTTTTTT-----DSRAGEEGSIRAVDHAVIGGVAV 383

Db 307 LPTTIIPSLTATVTTVAITTSPTTSATTSIRDPNALAGQNP----DHALLGGIVAV 362

QY 384 VVFAMLCILLIILORYFARHKGYTFHEAKGAADADADTAIINAEGSQVNAEKKEYFI 442

Db 363 VVFTLCSIFLLGRYLARHKGYTLTNEAKGAEDAPDADTAIINAEGSQVNAEKKEYFI 421

RESULT 9

US-09-778-510-4

; Sequence 4, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US

; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: PCT/US99/17906

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/095,663

; PRIOR FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-778-510-4

Query Match 32.7%; Score 745.5; DB 4; Length 398;

Best Local Similarity 39.1%; Pred. No. 3.7e-57;

Matches 172; Conservative 74; Mismatches 137; Indels 57; Gaps 11;

QY 16 AAAAAAPGLRLRLRLLLLFSAALIPGT-----DQNLFTKDVTVIEGAVATISQVKNKSD 70

Db 3 APAASP-----VPLLLLL--ACSWAPGGANLSQDSDQPTSDTETVWAGTVVLKQVKDHE 56

QY 71 DSVIQLLNPNRTIYFDRPLKDSRFQLNFSSELKVSILTNVISDEGRYFCQLYTDP 130

Db 57 DSSLQSNPAQQTLYFGEKALRDNRILQVSSSTPHELISISINVALADEGEYTCISFTMP 116

QY 131 PQESYTTITVLVPPRNLMIDIQDVAEGEEIEVNCETAMASKPATITIRWPKGNTELKQ-K 189

Db 117 VRTAKSLVTVLGIPIQKPIITGYKSSLREKETATLNCQSSGSKPAAQLTWKGDQELHGDQ 176

QY 190 SEVEEWSK--MYTVTSQMLKVKHKEDDGVPIQVEHPAVTG-NLQTRYLEVQYKQVH 246

Db 177 TRIQEDPNGKTFTVSSSVSPQVTRDDGANIVGSVNHESLKGADRSQSRIEVLVYTPAM 236

QY 247 IQMTYPLQGLTRGDALCEALGKQPVMVTWVRVDDMPP---QHAVLSGPNLFINN 302

Db 237 IR---PEPAHPREGQKLLHCEGEGNPVPOQYVWVKEGSEPPPLKMTQESALIFP----F 288

QY 303 LNKTDNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPTTTTTTTTTTTTTTTTTTTTTITDSR 362

Db 289 LNKSDSGTYCTATSNMGSYTAFTLNVDPS---PVPSSSTV----- 329

QY 363 AGEESIRAVDHAVIGGVAVVFPAMCLLIILGRVFAHKGTYFTHAEKGAADADADT 422

Db 330 -----HAIIGGIVAFIVFLLLIILIFLGHYLIIRHKGYTLTHEAKGSDADPADT 378

QY 423 AIINAEGSQVNAEKKEYFI 442

Db 379 AIINAEGSQSGDDKKEYFI 398

RESULT 10

US-09-778-510-6

; Sequence 6, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:


```
/ STREET: Two Embarcadero Ctr., 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/660,531
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/480,498
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heslin, James M.
/ REGISTRATION NUMBER: 29,541
/ REFERENCE/DOCKET NUMBER: 15270-002210US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-660-531-5

Query Match 39.5%; Score 902; DB 3; Length 444;
Best Local Similarity 44.6%; Pred. No. 8.3e-71;
Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

QY 31 LLFSAAA--LIPTDGGQLFTKQVTVIEGEVATISQVKNKSDSDSVIQLNPNRQTIYFR 87
Db 17 LLLQAASKNVKGSGQGFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWNPAAQTLTYFD 76

QY 88 DFRPLKDSRFOLLNFSSELKVLSTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPNRL 147
Db 77 DKKALDRNRIELVRASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKP 136

QY 148 MIDIQKTAVAGEEELVNCTAMASKPATTIRWFGKNTLKGKSEVEEWS---DMYTVTSQ 204
Db 137 QISGSSPVMGDLMLQCTKSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVST 196

QY 205 LMLVKHKEDDGVPVLCQVEHPAVTGNLQ--TORYLEVOYKPVQHIQMTYPLQGLTREGDAL 263
Db 197 LDFVRSDSDGVAVICRYVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTFPFQEGQPL 253

QY 264 ELTCEAIKGPQPMVTVRVVDEM--PQHAVLSGPNLFNINLKNKTNGTYRCEASNIYVK 321
Db 254 ILTCESKGKPEPVLWTKDGELPDPDRNVVSGRELNLFLNKDNGTYRCEATNIGQ 313

QY 322 AHSYMLVYDPTPIPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 367
Db 314 SSAEYVLIVHDVNTLLPTTIPSLTATVTTVAITTSPTTSATTSIRDPNALAGQNG 373

QY 368 SIRAVDHAVIGGVANVVFAMLCILLGRYFARHKGTYFTHEAKGADDAADADTAIINA 427
Db 374 P----DHALLIGIVAVVFTLCSIFLLGRYLARHKGTYLTNEAKGADPADADTAIINA 429

QY 428 EGGQNNSEKKEFYI 442
Db 430 EGSQVNAEKEFYI 444

RESULT 7
US-08-659-984A-1
; Sequence 1, Application US/08659984A

; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-1

Query Match 39.2%; Score 895.5; DB 2; Length 421;
Best Local Similarity 45.1%; Pred. No. 2.9e-70;
Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 44 GONLFTKQVTVIEGEVATISQVKNKSDSDSVIQLNPNRQTIYFRDPLKDSRFOLLNFS 103
Db 10 GQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWNPAAQTLTYFDKKALDRNRIELVRAS 69

QY 104 SSELKVLSTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPNLMIDIQKTAVAGEEIE 163
Db 70 WHELISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSPPVMGDLMQ 129

QY 164 VNTAMASKPATTIRWFGKNTLKGKSEVEEWS---DMYTVTSQMLKVKHKEDDGVPVVC 220
Db 130 LTCTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSITLDFVRSDSDGVAVIC 189

QY 221 QVEHPAVTGNLQ--TORYLEVOYKPVQHIQMTYPLQGLTREGDALELTCEAIKGPQPMVT 279
Db 190 RVDSHESLNATPQVAMQVLEIHYTPSVKI---IPSTFPFQEGQPLILTCESKGKPLPEPVL 246

QY 280 WVRVDDM--PQHAVLSGPNLFNINLKNKTNGTYRCEASNIYVKHSDYMLVYVDDPTTI 337
Db 247 WTKDGELPDPDRNVVSGRELNLFLNKDNGTYRCEATNIGQSSAEYVLIVHDVNTLL 306

QY 338 PPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 383
Db 307 LPTTIIPSLTATVTTVAITTSPTTSATTSIRDPNALAGQNGP---DHALLIGIVAV 362

QY 384 VVFMALCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGQNNSEKKEFYI 442
Db 384 VVFMALCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGQNNSEKKEFYI 442
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; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match 95.0%; Score 2169; DB 4; Length 423;
Best Local Similarity 98.8%; Pred. No. 6.1e-182;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 19 AAPGRLRLRLLLLSAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
DB 1 AAPGRLRLRLLLLSAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
QY 79 PNRQTIYFRDPRPLKDSRFQLLNFSSELKVSNTNVSISDEGRYFCOLYTDPPQESYTTI 138
DB 61 PNRQTIYFRDPRPLKDSRFQLLNFSSELKVSNTNVSISDEGRYFCOLYTDPPQESYTTI 120
QY 139 TVLVPPRNLMIDIQKQTAVEGEIEVNTAMASKPATIRWFKGNTLKGKSEVEEWSDM 198
DB 121 TVLVPPRNLMIDIQKQTAVEGEIEVNTAMASKPATIRWFKGNTLKGKSEVEEWSDM 180
QY 199 YTVTSQMLVKHEDDGVPIQVEHEPAVTGNLTQRYLEVQYKPVQHIQMTYVLOGLTR 258
DB 181 YTVTSQMLVKHEDDGVPIQVEHEPAVTGNLTQRYLEVQYKPVQHIQMTYVLOGLTR 240
QY 259 EGDALFTCEAIGKPPQVMVTVRVDDEMPQHAVLSGNLFINNKNKTNGTYRCEASNI 318
DB 241 EGDALFTCEAIGKPPQVMVTVRVDDEMPQHAVLSGNLFINNKNKTNGTYRCEASNI 300
QY 319 VGKASDYMLYVDDPPTTIPPTTTTITITITITITITITITITITITITITITITITIT 378
DB 301 VGKASDYMLYVDDPPTTIPPTTTTITITITITITITITITITITITITITITITITIT 360
QY 379 GVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEQGNNEEKK 438
DB 361 GVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEQGNNEEKK 420
QY 439 EYF 441
DB 421 EYF 423

RESULT 5
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 39.5%; Score 902; DB 2; Length 444;
Best Local Similarity 44.6%; Pred. No. 8.3e-71;
Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

QY 31 LLFSAAA--LIFTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLNPNRQTIYFR 87
DB 17 LLQAAAANKVKGSGQGPLTONVTVIEGTAITLCRVDDNDNTSLQWSNPAQOTLYFD 76
QY 88 DFRPLKDSRFQLLNFSSELKVSNTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPRN 147
DB 77 DKALRDNRILVRAWHLSISVSDVSLSDGQYTCSLTFMPVKTSKAVLTVLGVPEKP 136
QY 148 MIDIQKQTAVEGEIEVNTAMASKPATIRWFKGNTLKGKSEVEEWS---DMYVTSQ 204
DB 137 QISGFSFVMEGLMQLTCKTSGSKPAADIRWFKNDKEIKDKVYLKEEDANRKTFTVST 196
QY 205 LMLKVHEDDGVPIQVEHEPAVTGNLQ-TQRYLEVQYKPVQHIQMTYVLOGLTREGDAL 263
DB 197 LDFRDRSDGAVICRVHESLNATPQAMQVLEIHYTESVKI---IPSTPPFQEQPL 253
QY 264 ELTCEAIGKPPQVMVTVRVDDEMPQHAVLSGNLFINNKNKTNGTYRCEASNIYVK 321
DB 254 ILTCESKGKPLPEPLVTKDGGELPDPRMVSREINILFNKTDNGTYRCEATWIGQ 313
QY 322 AHSIDMYLYVDDPPTTIPPTTTTITITITITITITITITITITITITITITITITIT 367
DB 314 SSAEYVLIYVHVDVENTLLPTTIIPSLTAITVTTVAITTSPTTSATTSIRDPNALAGQ 373
QY 368 STRAVDHAVIGGVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAE 427
DB 374 P-----DHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLITNEAKGADPADATAIIN 429
QY 428 EGGQNNSEKKEYFI 442
DB 430 EGSQVNAEKKKEYFI 444

RESULT 6
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP

Qy 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Qy 421 DTAIINAEAGGNNSEKKEYFI 442
Db 421 DTAIINAEAGGNNSEKKEYFI 442

RESULT 2

US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JH01770-1
; CURRENT APPLICATION NUMBER: US/09/930.803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 100.0%; Score 2283; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.6e-192;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPDGQNLFTKDVTVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPDGQNLFTKDVTVIEGEVA 60
Qy 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILNVSISDEG 120
Db 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILNVSISDEG 120
Qy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCATAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCATAMASKPATIRWF 180
Qy 181 KGNTLKGKSEVEWSDMYTVTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVEWSDMYTVTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Qy 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Qy 421 DTAIINAEAGGNNSEKKEYFI 442
Db 421 DTAIINAEAGGNNSEKKEYFI 442

RESULT 3

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866.028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 99.1%; Score 2263; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 3.7e-190;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPDGQNLFTKDVTVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPDGQNLFTKDVTVIEGEVA 58
Qy 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILNVSISDEG 120
Db 59 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILNVSISDEG 118
Qy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCATAMASKPATIRWF 180
Db 119 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCATAMASKPATIRWF 178
Qy 181 KGNTLKGKSEVEWSDMYTVTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Db 179 KGNTLKGKSEVEWSDMYTVTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 238
Qy 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGNLFI 300
Db 239 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGNLFI 298
Qy 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 299 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 358
Qy 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 359 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 418
Qy 421 DTAIINAEAGGNNSEKKEYFI 442
Db 419 DTAIINAEAGGNNSEKKEYFI 440

RESULT 4

US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 8512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778.510

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 16.1676 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-2

Perfect score: 2283
Sequence: 1 MASVLPSSGSCAAAAA.....AIINAEQGNNSSEKKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2283	100.0	442	4	US-09-778-510-20
2	2283	100.0	442	4	US-09-930-803-1
3	2263	99.1	440	4	US-09-866-028-61
4	2169	95.0	423	4	US-09-778-510-22
5	902	39.5	444	2	US-08-659-984A-5
6	902	39.5	444	3	US-08-660-531-5
7	895.5	39.2	421	2	US-08-659-984A-1
8	895.5	39.2	421	3	US-08-660-531-1
9	745.5	32.7	398	4	US-09-778-510-4
10	739	32.4	398	4	US-09-778-510-6
11	739	32.4	398	4	US-09-907-794A-84
12	739	32.4	398	4	US-09-905-125A-84
13	739	32.4	398	4	US-09-902-775A-84
14	722	31.6	432	4	US-09-778-510-2
15	335	14.7	227	4	US-09-205-358-947
16	256.5	11.2	517	4	US-09-723-368-4
17	248	10.9	518	4	US-09-919-172-20
18	232	10.2	393	1	US-08-439-742-2
19	226	9.9	479	4	US-09-723-368-2
20	222	9.7	458	4	US-09-435-956A-1
21	220.5	9.7	344	4	US-09-700-397-3
22	211	9.2	313	4	US-08-700-397-4
23	208	9.1	388	1	US-08-429-742-4
24	206	9.0	642	1	US-08-217-299-1
25	206	9.0	698	2	US-08-602-725-36
26	206	9.0	734	2	US-08-389-459A-17
27	206	9.0	734	3	US-08-987-867A-17

ALIGNMENTS

RESULT 1

US-09-778-510-20

; Sequence 20, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; TITLE OF INVENTION: Molecules Designated B711

; FILE REFERENCE: 2844-US

; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: PCT/US99/17906

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/095,663

; PRIOR FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-778-510-20

Query Match	100.0%;	Score 2283;	DB 4;	Length 442;
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Db	1	MASVLPSSGSCAAAAAAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVA	60	
Qy	61	TISCVNKSDDSVIQLNPNRQTIYFRDPLKDSFQLNFSSELKSLTNVSI	120	
Db	61	TISCVNKSDDSVIQLNPNRQTIYFRDPLKDSFQLNFSSELKSLTNVSI	120	
Qy	121	RYFCOLYTDPPQPSYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPAT	180	
Db	121	RYFCOLYTDPPQPSYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPAT	180	
Qy	181	KGNTLKGKSEVSEWSDMYTTSQMLKVHKKDDGVPIQCVHEHPAVTGNLQRYLEVQ	240	
Db	181	KGNTLKGKSEVSEWSDMYTTSQMLKVHKKDDGVPIQCVHEHPAVTGNLQRYLEVQ	240	
Qy	241	YKQVHIQMTYPIQGLTREGDALELCEAIGKQPMVTVWRVDDDEMPQHAVLSGPNLFI	300	
Db	241	YKQVHIQMTYPIQGLTREGDALELCEAIGKQPMVTVWRVDDDEMPQHAVLSGPNLFI	300	
Qy	301	NNLNKTDNGTYRCEASNIVGKASHDYMVYVDPPTTIPPTTTTTTTTTTTTTTTTT	360	
Db	301	NNLNKTDNGTYRCEASNIVGKASHDYMVYVDPPTTIPPTTTTTTTTTTTTTTTTT	360	

Best Local Similarity 99.5%; Pred. No. 3.4e-175;			
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
Qy	1	MASVVLPSGSCACAAAAAAPPGLRLRLLLLSAAALIP	60
Db	1	MASVVLPSGSCACAAAAAAPPGLRLRLLLLSAAALIP	58
Qy	61	TISQVVKSDSVIQLLNPQRQTIYFRDRPLKDSRFOLLN	120
Db	59	TISQVVKSDSVIQLLNPQRQTIYFRDRPLKDSRFOLLN	118
Qy	121	RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKOTAVE	180
Db	119	RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKOTAVE	178
Qy	181	KGNTLKGKSEVEEWSDMYTVTSQLMLKVHKEDDGPV	240
Db	179	KGNTLKGKSEVEEWSDMYTVTSQLMLKVHKEDDGPV	238
Qy	241	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPVM	300
Db	239	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPVM	298
Qy	301	NNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPPPT	360
Db	299	NNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPPPT	358
Qy	361	SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGR	420
Db	359	SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGR	418
Qy	421	DTAIINAEQQNNSEEKEYFI	442
Db	419	DTAIINAEQQNNSEEKEYFI	440

Search completed: May 27, 2004, 09:52:20
Job time : 39.5504 secs

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy 61 TISQVKNKSDSVIQLLNPQRQTIYFRDPLKDSRFOLLNFSSELKVSILTNVISIDEG 120
Db 59 TISQVKNKSDSVIQLLNPQRQTIYFRDPLKDSRFOLLNFSSELKVSILTNVISIDEG 118
Qy 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIEVNCNTAMASKPATIRWF 180
Db 119 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIEVNCNTAMASKPATIRWF 178
Qy 181 KGNTELKGSSEWSDMYTTSOLMLKVHEDGVPVICOVEHPAVTGNLQORYLEVQ 240
Db 179 KGNTELKGSSEWSDMYTTSOLMLKVHEDGVPVICOVEHPAVTGNLQORYLEVQ 238
Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIKGPQFVMVTVVRVDEMPQHAVLSPNLI 300
Db 239 YKPOVHIQMTYPLQGLTREGDALELTCEAIKGPQFVMVTVVRVDEMPQHAVLSPNLI 298
Qy 301 NNLKNTDNGTYRCASNIIVGAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 299 NNLKNTDNGTYRCASNIIVGAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 358
Qy 361 SRAGEGSIRAVDHAVIGGVVVVVFAMLCLLIILGRYFARHKTYTFHEAKGADDAADA 420
Db 359 SRAGEGSIRAVDHAVIGGVVVVVFAMLCLLIILGRYFARHKTYTFHEAKGADDAADA 418
Qy 421 DTAIINAEQQNNSEKKEYPI 442
Db 419 DTAIINAEQQNNSEKKEYPI 440

RESULT 15
US-09-945-015-61
; Sequence 61, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

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; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,596
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-015-61

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Query Match

99.1%; Score 2263; DB 9; Length 440;

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Db	59 TISQVNVKSDSVIQLLNPNRQTIYFRDRLKDSRFOLLNFSSSELKVSILTNVSIISDEG 118
QY	121 RYFQCLYDPPQESYTTITVLVPPRNLMIDIQKOTAVEGEBIEVNCAMASKPATIRWF 180
Db	119 RYFQCLYDPPQESYTTITVLVPPRNLMIDIQKOTAVEGEBIEVNCAMASKPATIRWF 178
QY	181 KGNTLKGKSEVSWSDMYTTSQMLMKVHKEDDGPVICOVEHPATGNLTQORYLEVQ 240
Db	179 KGNTLKGKSEVSWSDMYTTSQMLMKVHKEDDGPVICOVEHPATGNLTQORYLEVQ 238
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QY	361 SRAGEEGSIRAVDHAVIGGVVAVVVFVAMLCILILGRYFARHKGTFTHEAKGADDAADA 420
Db	359 SRAGEEGSIRAVDHAVIGGVVAVVVFVAMLCILILGRYFARHKGTFTHEAKGADDAADA 418
QY	421 DTAIINAEGQNNSEKKEYFI 442
Db	419 DTAIINAEGQNNSEKKEYFI 440
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; Sequence 61, Application US/09945587	
; Patent No. US20020127643A1	
; GENERAL INFORMATION:	
; APPLICANT: Baker, Kevin	
; APPLICANT: Botstein, David	
; APPLICANT: Eaton, Dan	
; APPLICANT: Ferrara, Napoleone	
; APPLICANT: Filvaroff, Ellen	
; APPLICANT: Gerritsen, Mary	
; APPLICANT: Goddard, Audrey	
; APPLICANT: Godowski, Paul	
; APPLICANT: Grimaldi, Christopher	
; APPLICANT: Gurney, Austin	
; APPLICANT: Hillan, Kenneth	
; APPLICANT: Kljavin, Ivar	
; APPLICANT: Napier, Mary	
; APPLICANT: Roy, Margaret	
; APPLICANT: Tumas, Daniel	
; APPLICANT: Wood, William	
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	
; FILE REFERENCE: P2548P1C1	
; CURRENT APPLICATION NUMBER: US/09/945,587	
; CURRENT FILING DATE: 2001-09-26	
; PRIOR APPLICATION NUMBER: 09/866,028	
; PRIOR FILING DATE: 2001-05-25	
; PRIOR APPLICATION NUMBER: 60/067,411	
; PRIOR FILING DATE: December 3, 1997	
; PRIOR APPLICATION NUMBER: 60/069,334	
; PRIOR FILING DATE: December 11, 1997	
; PRIOR APPLICATION NUMBER: 60/069,335	
; PRIOR FILING DATE: December 11, 1997	
; PRIOR APPLICATION NUMBER: 60/069,278	
; PRIOR FILING DATE: December 11, 1997	
; PRIOR APPLICATION NUMBER: 60/069,425	

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDGNLFTKDVTVIEGVA 58
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DB 59 TISQVKNKSDSVIQLLNPQRQTIYFRDPLKDSRFQLLNPSSELKVSILNVSISDEG 118
QY 121 RYFQCLYTRDPQESYTTITLVVPRNLMIDIKOTAVEGEEIEVNCVTAMASKPATIRWF 180
DB 119 RYFQCLYTRDPQESYTTITLVVPRNLMIDIKOTAVEGEEIEVNCVTAMASKPATIRWF 178
QY 181 KGNTLKGKSVBEWSDMYTYSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYLEVQ 240
DB 179 KGNTLKGKSVBEWSDMYTYSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYLEVQ 238
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTWVRVDEMPQHAVLSGPNLFI 300
DB 239 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTWVRVDEMPQHAVLSGPNLFI 298
QY 301 NNLKNTDNGTYRCASNIYVGAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTT 360
DB 299 NNLKNTDNGTYRCASNIYVGAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFVAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
DB 359 SRAGEGSIRAVDHAVIGGVAVVVFVAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
QY 421 DTAINAEGGQNNSEKKEYFI 442
DB 419 DTAINAEGGQNNSEKKEYFI 440

RESULT 13
US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 15, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-862-61

Query Match 99.1%; Score 2263; DB 9; Length 440;
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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCCAAAAAAAGPLRLRLLLLSAALIPGTGDNLFKDVTVIEGVA 60
Db 1 MASVVLPSGSCCAAAAAAAGPLRLRLLLLSAALIPGTGDNLFKDVTVIEGVA 58
QY 61 TISCVNKSDDSVIQLLNPNTQIYFRDPRPLKDSRFQLLNFSSSELKVSNTNVSISDEG 120
Db 59 TISCVNKSDDSVIQLLNPNTQIYFRDPRPLKDSRFQLLNFSSSELKVSNTNVSISDEG 118
QY 121 RYFCOLYTDPPQESYTTITVLVPPNLMIDIKOTAVEGEBIEVNCNTAMAKPATIRWF 180
Db 119 RYFCOLYTDPPQESYTTITVLVPPNLMIDIKOTAVEGEBIEVNCNTAMAKPATIRWF 178
QY 181 KGNTELKSKSEVEWSDMYTTSQMLKVKHKEDDGVVICQVEHPAVTGNLQTKRYLEVQ 240
Db 179 KGNTELKSKSEVEWSDMYTTSQMLKVKHKEDDGVVICQVEHPAVTGNLQTKRYLEVQ 238
QY 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSPNLF 300
Db 239 YKPOVHIOMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSPNLF 298
QY 301 NNLKNTDNGTYRCASNTVGVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
Db 299 NNLKNTDNGTYRCASNTVGVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGYTFTHAKGADDAADA 420
Db 359 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGYTFTHAKGADDAADA 418
QY 421 DTAIINAEAGGQNNSEKKEYFI 442
Db 419 DTAIINAEAGGQNNSEKKEYFI 440

RESULT 12
US-09-944-457-61
; Sequence 61, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivartoff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-457-61

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCAAAAAAPGLRLRLLLLSAALIPITGDGQNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPG--LRULLLLLSAALIPITGDGQNLFTKDVTVIEGEVA 58
QY 61 TISCVNKSDDSVIQLLPNRTIIFRPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
Db 59 TISCVNKSDDSVIQLLPNRTIIFRPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 118
QY 121 RYFCQLYTDPPQESYTTITLVLPNRLMIDIKDTAVGEELEVNCTAMASKPATIIEWF 180
Db 119 RYFCQLYTDPPQESYTTITLVLPNRLMIDIKDTAVGEELEVNCTAMASKPATIIEWF 178
QY 181 KGNTELKKGSEVEENSDMYTTSVLSQLMLKVHKEDDGPVICOVEHPAVTGNLTQRYLEVQ 240
Db 179 KGNTELKKGSEVEENSDMYTTSVLSQLMLKVHKEDDGPVICOVEHPAVTGNLTQRYLEVQ 238
QY 241 YKPOVHIQMTYPLQGLTBEGDALELTCEAIGKQPQVMVTVRVDDDEMPQHAVLSGPNLFI 300
Db 239 YKPOVHIQMTYPLQGLTBEGDALELTCEAIGKQPQVMVTVRVDDDEMPQHAVLSGPNLFI 298
QY 301 NNINKTNGTYRCEASNIYVGRKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTLT 360
Db 299 NNINKTNGTYRCEASNIYVGRKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTLT 358
QY 361 SRAGEGSIKRAVDHAGVIGVAVVVFAMCLLIILGRYFARHKGYFTHEAKGADDAADA 420
Db 359 SRAGEGSIKRAVDHAGVIGVAVVVFAMCLLIILGRYFARHKGYFTHEAKGADDAADA 418
QY 421 DTAIINAEAGGQNNSEKKEYFI 442
Db 419 DTAIINAEAGGQNNSEKKEYFI 440

RESULT 11
US-09-944-449-61
; Sequence 61, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944.449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,236
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-449-61
Query Match 99.1%; Score 2263; DB 9; Length 440;
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QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
QY 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVHKEDDGPVPIQVEHPAVTGNLQTOXYLEVQ 240
Db 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVHKEDDGPVPIQVEHPAVTGNLQTOXYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDDMPQHAVLSGPNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
QY 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
QY 421 DTAIINAEGGQNNSEKKEYFI 442
Db 421 DTAIINAEGGQNNSEKKEYFI 442
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RESULT 9

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US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110
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Query Match 99.8%; Score 2280; DB 15; Length 442;
Best Local Similarity 99.8%; Pred. No. 1.4e-176;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVLPFSGSQCAAAAAAPPGLRLRLRLLLLSAAALIFTGQONLFTKDVTVIEGEVA 60
Db 1 MASVLPFSGSQCAAAAAAPPGLRLRLRLLLLSAAALIFTGQONLFTKDVTVIEGEVA 60
QY 61 TISCQVKNKSDSDSVIQLLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
Db 61 TISCQVKNKSDSDSVIQLLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
QY 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVHKEDDGPVPIQVEHPAVTGNLQTOXYLEVQ 240
Db 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVHKEDDGPVPIQVEHPAVTGNLQTOXYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDDMPQHAVLSGPNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
QY 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
QY 421 DTAIINAEGGQNNSEKKEYFI 442
Db 421 DTAIINAEGGQNNSEKKEYFI 442
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RESULT 10

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US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PPT
; ORGANISM: Homo Sapien
US-09-866-028-61
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Query Match

99.1%; Score 2263; DB 9; Length 440;

Db 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVA 60
Qy 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSILTNVISDEG 120
Db 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSILTNVISDEG 120
Qy 121 RYFCQLYTDPQESVTTITLVLPNRLMIDIKDTAVEGEIEIENCTAMASKPATTIRWF 180
Db 121 RYFCQLYTDPQESVTTITLVLPNRLMIDIKDTAVEGEIEIENCTAMASKPATTIRWF 180
Qy 181 KGNTLKGKSEVEEWSMDYTTVTSOLMLKVHKEDDGVPIQVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVEEWSMDYTTVTSOLMLKVHKEDDGVPIQVEHPAVTGNLQORYLEVQ 240
Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDEMPQHAVLSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDEMPQHAVLSGPNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Qy 421 DTAIINAEAGGQNNSEKKEYFI 442
Db 421 DTAIINAEAGGQNNSEKKEYFI 442

RESULT 7

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Murakami
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403.107
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVA 60
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Db 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSILTNVISDEG 120
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Db 121 RYFCQLYTDPQESVTTITLVLPNRLMIDIKDTAVEGEIEIENCTAMASKPATTIRWF 180
Qy 181 KGNTLKGKSEVEEWSMDYTTVTSOLMLKVHKEDDGVPIQVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVEEWSMDYTTVTSOLMLKVHKEDDGVPIQVEHPAVTGNLQORYLEVQ 240

Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDEMPQHAVLSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDEMPQHAVLSGPNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Qy 421 DTAIINAEAGGQNNSEKKEYFI 442
Db 421 DTAIINAEAGGQNNSEKKEYFI 442

RESULT 8

US-10-015-115-111
; Sequence 111, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match 100.0%; Score 2283; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVA 60
Qy 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSILTNVISDEG 120

RESULT 4

US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-136

Query Match 100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAL	IP	TGQNL	FTKDV	TVIEGEVA	60
DB	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAL	IP	TGQNL	FTKDV	TVIEGEVA	60
QY	61	TISQV	NKSDSV	LIQLN	PNRQ	TIY	FRD	FRPL	KDSR	PQLN	FSSELK
DB	61	TISQV	NKSDSV	LIQLN	PNRQ	TIY	FRD	FRPL	KDSR	PQLN	FSSELK
QY	121	RYFCQ	LYTDP	PQESY	TTIVL	VP	PNLM	IDIQ	KDTA	VEGE	IEIVNCTA
DB	121	RYFCQ	LYTDP	PQESY	TTIVL	VP	PNLM	IDIQ	KDTA	VEGE	IEIVNCTA
QY	181	KGNTL	KGKSE	VEWSD	MTVT	TSQ	MLKV	HKED	DGVP	VICQ	VEHPAV
DB	181	KGNTL	KGKSE	VEWSD	MTVT	TSQ	MLKV	HKED	DGVP	VICQ	VEHPAV
QY	241	YKQV	HIQMT	YP	LOGL	TREG	DALE	LTCE	ALGK	POPM	VTVR
DB	241	YKQV	HIQMT	YP	LOGL	TREG	DALE	LTCE	ALGK	POPM	VTVR
QY	301	NNLKT	DNGTYR	CEAS	NI	VGK	ASD	YMLV	YD	PTTIP	PP
DB	301	NNLKT	DNGTYR	CEAS	NI	VGK	ASD	YMLV	YD	PTTIP	PP
QY	361	SRAGE	SGS	IRAV	DH	AVIG	GV	VAVV	FAM	CLLI	ILGR
DB	361	SRAGE	SGS	IRAV	DH	AVIG	GV	VAVV	FAM	CLLI	ILGR
QY	421	DTAI	NAEG	QNN	SEK	KEYFI	442				
DB	421	DTAI	NAEG	QNN	SEK	KEYFI	442				

RESULT 5

US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hveeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262

Query Match 100.0%; Score 2283; DB 12; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAL	IP	TGQNL	FTKDV	TVIEGEVA	60
DB	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAL	IP	TGQNL	FTKDV	TVIEGEVA	60
QY	61	TISQV	NKSDSV	LIQLN	PNRQ	TIY	FRD	FRPL	KDSR	PQLN	FSSELK
DB	61	TISQV	NKSDSV	LIQLN	PNRQ	TIY	FRD	FRPL	KDSR	PQLN	FSSELK
QY	121	RYFCQ	LYTDP	PQESY	TTIVL	VP	PNLM	IDIQ	KDTA	VEGE	IEIVNCTA
DB	121	RYFCQ	LYTDP	PQESY	TTIVL	VP	PNLM	IDIQ	KDTA	VEGE	IEIVNCTA
QY	181	KGNTL	KGKSE	VEWSD	MTVT	TSQ	MLKV	HKED	DGVP	VICQ	VEHPAV
DB	181	KGNTL	KGKSE	VEWSD	MTVT	TSQ	MLKV	HKED	DGVP	VICQ	VEHPAV
QY	241	YKQV	HIQMT	YP	LOGL	TREG	DALE	LTCE	ALGK	POPM	VTVR
DB	241	YKQV	HIQMT	YP	LOGL	TREG	DALE	LTCE	ALGK	POPM	VTVR
QY	301	NNLKT	DNGTYR	CEAS	NI	VGK	ASD	YMLV	YD	PTTIP	PP
DB	301	NNLKT	DNGTYR	CEAS	NI	VGK	ASD	YMLV	YD	PTTIP	PP
QY	361	SRAGE	SGS	IRAV	DH	AVIG	GV	VAVV	FAM	CLLI	ILGR
DB	361	SRAGE	SGS	IRAV	DH	AVIG	GV	VAVV	FAM	CLLI	ILGR
QY	421	DTAI	NAEG	QNN	SEK	KEYFI	442				
DB	421	DTAI	NAEG	QNN	SEK	KEYFI	442				

RESULT 6

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US2003014478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
Db 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
QY 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
Db 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
QY 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442
RESULT 2
US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Faselow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2
Query Match 100.0%; Score 2283; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLSAAALIPGTGQNLPTKDVTVIEGEVA 60
QY 61 TISQVKNKSDSVIQLNPNRQTIYFRDPRPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
Db 61 TISQVKNKSDSVIQLNPNRQTIYFRDPRPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCCTAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCCTAMASKPATIRWF 180
QY 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
Db 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
QY 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
Db 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420

Db 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
QY 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442
RESULT 3
US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-136
Query Match 100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 TISQVKNKSDSVIQLNPNRQTIYFRDPRPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCCTAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCCTAMASKPATIRWF 180
QY 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
Db 181 KNTLKGKSEVEWSDMYTTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
QY 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
Db 241 YKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTWVRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDGTYRCEASNIQVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
QY 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 37.5504 Seconds
(without alignments)
3286.999 Million cell updates/sec

Title: US-09-778-187B-2

Perfect score: 2283

Sequence: 1 MASVLPSSGSCQCAAAAAA.....AIINAEQQNSSEKKEYFI 442

Scoring table: BLOSUM62

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Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2283	100.0	442	9	US-09-778-510-20
2	2283	100.0	442	9	US-09-778-187B-2
3	2283	100.0	442	10	US-09-984-130-136
4	2283	100.0	442	10	US-09-836-353A-136
5	2283	100.0	442	12	US-10-363-616-262
6	2283	100.0	442	14	US-10-302-041-20
7	2283	100.0	442	14	US-10-403-107-1
8	2283	100.0	442	15	US-10-015-115-111
9	2280	99.9	442	15	US-10-015-115-110
10	2263	99.1	440	9	US-09-866-028-61
11	2263	99.1	440	9	US-09-944-449-61
12	2263	99.1	440	9	US-09-944-457-61
13	2263	99.1	440	9	US-09-944-862-61
14	2263	99.1	440	9	US-09-945-587-61
15	2263	99.1	440	9	US-09-945-015-61

16	2263	99.1	440	9	US-09-944-396-61	Sequence 61, Appl
17	2263	99.1	440	9	US-09-944-097-61	Sequence 61, Appl
18	2263	99.1	440	9	US-09-944-432-61	Sequence 61, Appl
19	2263	99.1	440	9	US-09-943-762-61	Sequence 61, Appl
20	2263	99.1	440	9	US-09-944-654-61	Sequence 61, Appl
21	2263	99.1	440	9	US-09-943-851A-61	Sequence 61, Appl
22	2263	99.1	440	9	US-09-944-413-61	Sequence 61, Appl
23	2263	99.1	440	9	US-09-944-403-61	Sequence 61, Appl
24	2263	99.1	440	9	US-09-944-896-61	Sequence 61, Appl
25	2263	99.1	440	9	US-09-944-944-61	Sequence 61, Appl
26	2263	99.1	440	9	US-09-944-929-61	Sequence 61, Appl
27	2263	99.1	440	9	US-09-944-907-61	Sequence 61, Appl
28	2263	99.1	440	10	US-09-944-884-61	Sequence 61, Appl
29	2263	99.1	440	10	US-09-944-852-61	Sequence 61, Appl
30	2263	99.1	440	10	US-09-943-780-61	Sequence 61, Appl
31	2263	99.1	440	11	US-09-945-584-61	Sequence 61, Appl
32	2263	99.1	440	12	US-10-206-915-34	Sequence 34, Appl
33	2263	99.1	440	12	US-10-199-670-34	Sequence 34, Appl
34	2263	99.1	440	12	US-10-201-858-34	Sequence 34, Appl
35	2263	99.1	440	12	US-10-205-890-34	Sequence 34, Appl
36	2263	99.1	440	12	US-10-208-024-34	Sequence 34, Appl
37	2263	99.1	440	12	US-10-201-853-34	Sequence 34, Appl
38	2263	99.1	440	12	US-10-677-471-61	Sequence 61, Appl
39	2263	99.1	440	12	US-10-677-669-61	Sequence 61, Appl
40	2263	99.1	440	12	US-10-174-581-34	Sequence 34, Appl
41	2263	99.1	440	12	US-10-176-483-34	Sequence 34, Appl
42	2263	99.1	440	12	US-10-176-749-34	Sequence 34, Appl
43	2263	99.1	440	12	US-10-176-914-34	Sequence 34, Appl
44	2263	99.1	440	12	US-10-176-915-34	Sequence 34, Appl
45	2263	99.1	440	12	US-10-176-484-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match 100.0%; Score 2283; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASVLPSSGSCQCAAAAAAAPPGLRLRLLLLFSAALPTGQGNLTKDVTVEGEVA	60
Db	1	MASVLPSSGSCQCAAAAAAAPPGLRLRLLLLFSAALPTGQGNLTKDVTVEGEVA	60
QY	61	TTSCQNKSDSDSVIQLNPNRQTIYFRDPRPKDSFQNLNFSSELKSLVLTNVSISDEG	120
Db	61	TTSCQNKSDSDSVIQLNPNRQTIYFRDPRPKDSFQNLNFSSELKSLVLTNVSISDEG	120
QY	121	RYFCQLYTDPPQESYTTITVLVPPRNLMDIQDIAVEGEEIEVNCTAMASKPATIRWF	180
Db	121	RYFCQLYTDPPQESYTTITVLVPPRNLMDIQDIAVEGEEIEVNCTAMASKPATIRWF	180

Qy	121	RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCNAMASKPATTTIRWF	180
Db	119	RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCNAMASKPATTTIRWF	178
Qy	181	KGNTLKGKSEVEWSDMYTVTSQMLKVKHKKDDGVPVICOVEHPAVTGNLQORYLEVQ	240
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Qy	241	YKPQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVVMVTVRVDDDEMPQHAVLSGPNLFI	300
Db	239	YKPQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVVMVTVRVDDDEMPQHAVLSGPNLFI	298
Qy	301	NNLAKTNGTYRCEASNIVGKAHSDYMLYVYDPPPTTTTTPPTTTTITITD	360
Db	299	NNLAKTNGTYRCEASNIVGKAHSDYMLYVYDPPPTTTTTPPTTTTITITD	358
Qy	361	SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHKAGDAADA	420
Db	359	SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGTYFTHKAGDAADA	418
Qy	421	DTAIINAFGGQNNSEKKEYFI	442
Db	419	DTAIINAFGGQNNSEKKEYFI	440

Search completed: May 27, 2004, 09:31:22
Job time : 54.588 secs

[illegible]

PT Nucleic acids encoding PRO secreted and transmembrane proteins.
 XX Claim 12; Fig 27; 123pp; English.
 XX The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
 XX Sequence 440 AA;
 SQ

Query Match 99.1%; Score 2263; DB 2; Length 440;
 Best Local Similarity 99.5%; Pred. No. 1.7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVA 60
 DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVA 58
 QY 61 TISCVNKSDDSVTLQNLNPKRTIYDFRPLKDSRFQLNFSSELKVSILTVNISDEG 120
 DB 59 TISCVNKSDDSVTLQNLNPKRTIYDFRPLKDSRFQLNFSSELKVSILTVNISDEG 118
 QY 121 RYFCQLYDTPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWF 180
 DB 119 RYFCQLYDTPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWF 178
 QY 181 KGNTELKGSVEVSWDMYVTSQMLKVKHKEDGVPVICQVEHPAVTGNLQTVLEVQ 240
 DB 179 KGNTELKGSVEVSWDMYVTSQMLKVKHKEDGVPVICQVEHPAVTGNLQTVLEVQ 238
 QY 241 YKQVHLQMTYPIQLGTFREGDALELTCEALGKQPQVWVTVRVDDEMPQHAVLSGNLFI 300
 DB 239 YKQVHLQMTYPIQLGTFREGDALELTCEALGKQPQVWVTVRVDDEMPQHAVLSGNLFI 298
 QY 301 NNLNKTDTNGTYRCEASNIIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTILITD 360
 DB 299 NNLNKTDTNGTYRCEASNIIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTILITD 358
 QY 361 SRAGEGSTRANDHANTGGVAVVVFAMLCILILGRYFARHKGTYPTHEAKGADDAADA 420
 DB 359 SRAGEGSTRANDHANTGGVAVVVFAMLCILILGRYFARHKGTYPTHEAKGADDAADA 418
 QY 421 DTAIINAEGQNNSEKKEYFI 442
 DB 419 DTAIINAEGQNNSEKKEYFI 440

RESULT 14
 AAB01321
 ID AAB01321 standard; protein; 440 AA.
 XX
 AC AAB01321;
 XX
 XX 25-SEP-2000 (first entry)
 XX
 DE Human PRO355 polypeptide.
 XX
 KW PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
 KW PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353;
 KW PRO361; PRO365; transmembrane polypeptide; antibody; screening;
 KW detection; inhibition; probe; primer; human.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..36 /label= Signal peptide
 FT Modified-site 9..15

FT Modified-site /note= "N-myristoylation site"
 FT 65..69
 FT /note= "N-glycosylation site"
 FT 99..103
 FT /note= "N-glycosylation site"
 FT 111..115
 FT /note= "N-glycosylation site"
 FT 163..167
 FT /note= "N-glycosylation site"
 FT 227..233
 FT /note= "N-myristoylation site"
 FT 233..240
 FT /note= "Tyrosine kinase phosphorylation site"
 FT 302..306
 FT /note= "N-glycosylation site"
 FT 306..310
 FT /note= "N-glycosylation site"
 FT 307..313
 FT /note= "N-myristoylation site"
 FT 319..328
 FT /note= "Tyrosine kinase phosphorylation site"
 FT 365..371
 FT /note= "N-myristoylation site"
 FT 372..393
 FT /label= Transmembrane domain
 FT 376..382
 FT /note= "N-myristoylation site"
 FT 402..408
 FT /note= "N-myristoylation site"
 FT 411..417
 FT /note= "N-myristoylation site"
 FT 427..433
 FT /note= "N-myristoylation site"
 FT 428..432
 FT /note= "N-myristoylation site"
 FT 430..434
 FT /note= "N-glycosylation site"
 XX
 PN WO200032776-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-US028301.
 XX
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0113296P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen MB, Goddard A, Godowski RJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kijavini LJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2000-412324/35.
 DR N-PSDB; AAA49563.
 XX
 PT New human nucleic acids encoding secreted and transmembrane polypeptides,
 PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
 PT agents.
 XX
 PS Claim 12; Fig 24; 187pp; English.
 XX
 CC New human nucleic acids encoding secreted and transmembrane polypeptides
 CC which are designated as PRO polypeptides are described. The membrane-bound
 CC proteins have various industrial applications, including as
 CC pharmaceutical and diagnostic agents. The membrane-bound proteins can
 CC also be employed for screening of potential peptide or small molecule
 CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO
 CC antibodies are useful for the affinity purification of PRO from
 CC recombinant cell culture or natural sources
 XX
 XX Sequence 440 AA;

AC ADE61608;
 XX 29-JAN-2004 (first entry)
 XX Human Protein AAF69029, SEQ ID NO 7528.
 XX Human; pain; neuronal tissue; gene therapy;
 XX spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX W02003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-033347P.
 XX (GEO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-269312/26.
 XX GENBANK; AAF69029.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 XX human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
 XX comprising the vector, a method for identifying a nucleotide sequence
 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially expressed in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 XX therapy). The sequence presented is a human protein (shown in table 2 of
 XX the specification) which is differentially expressed during pain. Note:
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 442 AA;
 XX
 XX Query Match 99.9%; Score 2280; DB 7; Length 442;
 XX Best Local Similarity 99.8%; Pred. No. 9.6e-158;
 XX Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLLFSAALIPGTGQCNLFKDVTVIEGEVA 60
 XX |
 XX 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLLFSAALIPGTGQCNLFKDVTVIEGEVA 60
 XX |

QY 61 TISCQVKNKSDSVIQLLNPNROTIIYFRDPRPLKDSRFQLLNFSSELKVLSTNVISDSDEG 120
 DB 61 TISCQVKNKSDSVIQLLNPNROTIIYFRDPRPLKDSRFQLLNFSSELKVLSTNVISDSDEG 120
 QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIIOKTAVEGEEIEVNCTANASKPATIRWF 180
 DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIIOKTAVEGEEIEVNCTANASKPATIRWF 180
 QY 181 KGNTELKSGKSEVEEWSDMYTVTSQMLMKVHKEDDGVFVICQVEHFAVTGNLQORYLEYQ 240
 DB 181 KGNTELKSGKSEVEEWSDMYTVTSQMLMKVHKEDDGVFVICQVEHFAVTGNLQORYLEYQ 240
 QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKPOPMVMTWVRVDDMPQHAVLSGNLFI 300
 DB 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKPOPMVMTWVRVDDMPQHAVLSGNLFI 300
 QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTIITD 360
 DB 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTIITD 360
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCILHILGRYFARHKGTPTTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCILHILGRYFARHKGTPTTHEAKGADDAADA 420
 QY 421 DTAIINAEQGNNSSEKKEYFI 442
 DB 421 DTAIINAEQGNNSSEKKEYFI 442
 RESULT 13
 AAY17830
 ID AAY17830 standard; protein; 440 AA.
 XX AC AAY17830;
 XX DT 12-AUG-1999 (first entry)
 XX DE Human PRO355 protein sequence.
 XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 XX KW secreted protein; transmembrane protein; inflammation disorder.
 XX OS Homo sapiens.
 XX DN W09928462-A2.
 XX PD 10-JUN-1999.
 XX PF 01-DEC-1998; 98WO-US025108.
 XX PR 03-DEC-1997; 97US-0067411P.
 XX PR 11-DEC-1997; 97US-0069278P.
 XX PR 11-DEC-1997; 97US-0069334P.
 XX PR 12-DEC-1997; 97US-0069335P.
 XX PR 16-DEC-1997; 97US-0069425P.
 XX PR 16-DEC-1997; 97US-0069694P.
 XX PR 16-DEC-1997; 97US-0069696P.
 XX PR 17-DEC-1997; 97US-0069702P.
 XX PR 17-DEC-1997; 97US-0069870P.
 XX PR 18-DEC-1997; 97US-0069873P.
 XX PR 05-JAN-1998; 98US-0070440P.
 XX PR 03-FEB-1998; 98US-0074086P.
 XX PR 03-FEB-1998; 98US-0074092P.
 XX PR 25-FEB-1998; 98US-0075945P.
 XX (GETH) GENENTECH INC.
 XX PA Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
 XX WPI; 1999-371118/31.
 XX N-PSDB; AAX80055.
 XX

Best Local Similarity 99.8%; Pred. No. 9.6e-158;		Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVA	60
Db	1	MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVA	60
QY	61	TISCQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG	120
Db	61	TISCQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG	120
QY	121	RYFCQLYTDPQBSYTTITVLVPPRNLMDIQDRTAVEGEIEVNCCTAMASKPATIRWF	180
Db	121	RYFCQLYTDPQBSYTTITVLVPPRNLMDIQDRTAVEGEIEVNCCTAMASKPATIRWF	180
QY	181	KGNTLKGKSEVEEWSDMYVTTSQMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ	240
Db	181	KGNTLKGKSEVEEWSDMYVTTSQMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ	240
QY	241	YKQVHIQMTYPIQGLTREGDALELTCEALGKQPPVMTWRVDDENPQHAVLSGNLFI	300
Db	241	YKQVHIQMTYPIQGLTREGDALELTCEALGKQPPVMTWRVDDENPQHAVLSGNLFI	300
QY	301	NNLKTNDNGTYRCEASNIVGKHSYMLVYDPTTIPPTTTTTTTTTTTTTILITD	360
Db	301	NNLKTNDNGTYRCEASNIVGKHSYMLVYDPTTIPPTTTTTTTTTTTTTILITD	360
QY	361	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADA	420
Db	361	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADA	420
QY	421	DTAIINAEQQNNSEKKEYFI 442	
Db	421	DTAIINAEQQNNSEKKEYFI 442	
RESULT 11			
ADE61605 standard; protein; 442 AA.			
XX	AC	ADE61605;	
XX	DT	29-JAN-2004 (first entry)	
XX	DE	Human Protein AAF69029, SEQ ID NO 7525.	
XX	KW	Human; pain; neuronal tissue; gene therapy;	
XX	KW	spinal segmental nerve injury; chronic constriction injury; CCI;	
XX	OS	spared nerve injury; SNI; Chung.	
XX	OS	Homo sapiens.	
XX	PN	WO2003016475-A2.	
XX	PD	27-FEB-2003.	
XX	PF	14-AUG-2002; 2002WO-US025765.	
XX	PR	14-AUG-2001; 2001US-0312147P.	
XX	PR	01-NOV-2001; 2001US-0346382P.	
XX	PR	26-NOV-2001; 2001US-0333347P.	
XX	PA	(GEHO) GEN HOSPITAL CORP.	
XX	PA	(FARB) BAYER AG.	
XX	PI	Woolf C, D'urso D, Befort K, Costigan M;	
XX	PI	WPI; 2003-268312/26.	
XX	DR	GENBANK; AAF69029.	
XX	PT	New composition comprising two or more isolated polypeptides, useful for	
XX	PT	preparing a medicament for treating pain in an animal.	

PS	Claim 1; Page; 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC	therapy). The sequence presented is a human protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 442 AA;
	Query Match 99.9%; Score 2280; DB 7; Length 442;
	Best Local Similarity 99.8%; Pred. No. 9.6e-158;
	Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVA 60
Db	1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVA 60
QY	61 TISCQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
Db	61 TISCQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
QY	121 RYFCQLYTDPQBSYTTITVLVPPRNLMDIQDRTAVEGEIEVNCCTAMASKPATIRWF 180
Db	121 RYFCQLYTDPQBSYTTITVLVPPRNLMDIQDRTAVEGEIEVNCCTAMASKPATIRWF 180
QY	181 KGNTLKGKSEVEEWSDMYVTTSQMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ 240
Db	181 KGNTLKGKSEVEEWSDMYVTTSQMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ 240
QY	241 YKQVHIQMTYPIQGLTREGDALELTCEALGKQPPVMTWRVDDENPQHAVLSGNLFI 300
Db	241 YKQVHIQMTYPIQGLTREGDALELTCEALGKQPPVMTWRVDDENPQHAVLSGNLFI 300
QY	301>NNLKTNDNGTYRCEASNIVGKHSYMLVYDPTTIPPTTTTTTTTTTTTTILITD 360
Db	301>NNLKTNDNGTYRCEASNIVGKHSYMLVYDPTTIPPTTTTTTTTTTTTTILITD 360
QY	361>SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADA 420
Db	361>SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADA 420
QY	421>DTAIINAEQQNNSEKKEYFI 442
Db	421>DTAIINAEQQNNSEKKEYFI 442
RESULT 12	
ADE61608	standard; protein; 442 AA.
ID	
XX	

Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 QY 301 NNLNKTDNGTYRCEASNIYKHAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTTTTTIITD 360
 Db 301 NNLNKTDNGTYRCEASNIYKHAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTTTTTIITD 360
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 Db 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 QY 421 DTAINAEGGQNNSEKKEYFI 442
 Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 8
 ADE86685
 ID ADE86685 standard; protein; 442 AA.
 AC ADE86685;
 DT 29-JAN-2004 (first entry)
 DE Novel human secreted protein #11 associated protein #1.
 KW human; secreted protein; cancer; liver disorder; hepatitis;
 KW neural disorder; Alzheimer's disease.
 OS Homo sapiens.
 XX US2003129685-A1.
 PN 10-JUL-2003.
 XX 18-APR-2001; 2001US-00836353.
 XX 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99MO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX (NIJ/J) NI J.
 PA (YOUNG/) YOUNG P E.
 PA (KENN/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIY/) WEI Y.
 PA (GREE/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 XX Ni J, Young PE, Kenny JU, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM;
 XX WPI; 2004-020335/02.
 DR New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX Disclosure; SEQ ID NO 136; 380pp; English.
 PS The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 XX Sequence 442 AA;
 SQ Query Match 100.0%; Score 2283; DB 8; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALPTGQGNLFTKQDVTIVIEGVA 60
 Db 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALPTGQGNLFTKQDVTIVIEGVA 60
 QY 61 TISCQVNSDDSVIQLNPNRQTIYFRDPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
 Db 61 TISCQVNSDDSVIQLNPNRQTIYFRDPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
 QY 121 RYFCQLYTDPPQESYTTITLVPPRNLMDIOKDTAVEGEEIEVNCNTAMASKPATIRWF 180
 Db 121 RYFCQLYTDPPQESYTTITLVPPRNLMDIOKDTAVEGEEIEVNCNTAMASKPATIRWF 180
 QY 181 KGNTLKGKSEVEEWSMDMTVTTSQMLKVHKEDDGPVICOVEHPAVTGNLQRYLEVQ 240
 Db 181 KGNTLKGKSEVEEWSMDMTVTTSQMLKVHKEDDGPVICOVEHPAVTGNLQRYLEVQ 240
 QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 QY 301 NNLNKTDNGTYRCEASNIYKHAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTIITD 360
 Db 301 NNLNKTDNGTYRCEASNIYKHAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTIITD 360
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 Db 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 QY 421 DTAINAEGGQNNSEKKEYFI 442
 Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 9
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 XX ABO07196;
 XX 13-AUG-2003 (first entry)
 DT Human p53 modifying protein, SEQ ID 156.
 DE Human p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 XX antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX Homo sapiens.
 OS WO200209122-A1.
 PN 12-DEC-2002.
 XX 03-JUN-2002; 2002WO-US017382.
 XX 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-032805P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX (EXEL-) EXELIXIS INC.
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 DR WPI; 2003-156859/15.
 DR N-PSDB; ACD13371.
 XX Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.

in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the invention.

Sequence 442 AA;

Query Match	100.0.0%;	Score 2283;	DB 6;	Length 442;
Best Local Similarity	100.0.0%;	Pred. No. 5.8e-158;		
Matches 442;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MASVLPSSGSCAAAAAAPPGLRLRLLLLLLFSAAALPTGDCQNLFTKDVTVIEGEVA	60	
Db	1	MASVLPSSGSCAAAAAAPPGLRLRLLLLLLFSAAALPTGDCQNLFTKDVTVIEGEVA	60	
QY	61	TISQVKNKSDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSI	120	SDGE
Db	61	TISQVKNKSDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSI	120	SDGE
QY	121	RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEIYVNCVTAMASKPAT	180	TIRWF
Db	121	RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEIYVNCVTAMASKPAT	180	TIRWF
QY	181	KGNTLKGKSEVEBWSDMYITVTSQMLMKVHKEDDGPVICOVEHPAVTGNLQORYLE	240	QV
Db	181	KGNTLKGKSEVEBWSDMYITVTSQMLMKVHKEDDGPVICOVEHPAVTGNLQORYLE	240	QV
QY	241	YKQVHIQMTYPIQGLTRGDALELTCEATGKPOVMVTVRVVDEMPQHAVLSGNLFI	300	
Db	241	YKQVHIQMTYPIQGLTRGDALELTCEATGKPOVMVTVRVVDEMPQHAVLSGNLFI	300	
QY	301	NNLKTNDNGTYRCEASNVGKAHSDMYLYVDPPTTTTTTTTTTTTTTTTTLITITD	360	
Db	301	NNLKTNDNGTYRCEASNVGKAHSDMYLYVDPPTTTTTTTTTTTTTTTTTLITITD	360	
QY	361	SRAGEGSRADVHAVTGGVAVVVFVFAMLCLLIILGRYFAHKTGYTFHEAKGADDA	420	ADA
Db	361	SRAGEGSRADVHAVTGGVAVVVFVFAMLCLLIILGRYFAHKTGYTFHEAKGADDA	420	ADA
QY	421	DTAIINAEQQNNSEKKEYFI	442	
Db	421	DTAIINAEQQNNSEKKEYFI	442	

RESULT 7

RESOLUT
ADE54238

ID	ADE54238	standard:	protein:	442 AA.
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AC ADE54238;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP_055148, SEQ ID

XX

KW Human; pain; neu

MLM

KW YV

XX 5

yy

XXI

XX
NN

Y

PD	27-FEB-2003.	
XX		
PF	14-AUG-2002; 2002WO-US025765.	
XX		
XX		
PR	14-AUG-2001; 2001US-0312147P.	
PR	01-NOV-2001; 2001US-0346382P.	
PR	26-NOV-2001; 2001US-0333347P.	
XX		
PA	(GEO) GEN HOSPITAL CORP.	
PA	(FARB) BAYER AG.	
XX		
PI	Woolf C, D'urso D, Befort K, Costigan M;	
XX		
DR	WPI; 2C03-268312/26.	
DR	GENBANK; NP_055148.	
XX		
PT	New composition comprising two or more isolated polypeptides, useful for	
PT	preparing a medicament for treating pain in an animal.	
XX		
XX	Claim 1; Page; 1017pp; English.	
XX		
CC	The invention discloses a composition comprising two or more isolated rat	
CC	or human polynucleotides or a polynucleotide which represents a fragment,	
CC	derivative or allelic variation of the nucleic acid sequence. Also	
CC	claimed are a vector comprising the novel polynucleotide, a host cell	
CC	comprising the vector, a method for identifying a nucleotide sequence	
CC	which is differentially regulated in an animal subjected to pain and a	
CC	kit to perform the method, an array, a method for identifying an agent	
CC	that increases or decreases the expression of the polynucleotide sequence	
CC	that is differentially expressed in neuronal tissue of a first animal	
CC	subjected to pain, a method for identifying a compound which regulates	
CC	the expression of a polynucleotide sequence which is differentially	
CC	expressed in an animal subjected to pain, a method for identifying a	
CC	compound that regulates the activity of one or more of the	
CC	polynucleotides, a method for producing a pharmaceutical composition, a	
CC	method for identifying a compound or small molecule that regulates the	
CC	activity in an animal of one or more of the polypeptides given in the	
CC	specification, a method for identifying a compound useful in treating	
CC	pain and a pharmaceutical composition comprising the one or more	
CC	polypeptides or their antibodies. The polynucleotide or the compound that	
CC	modulates its activity is useful for preparing a medicament for treating	
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene	
CC	therapy). The sequence presented is a human protein (shown in Table 2 of	
CC	the specification) which is differentially expressed during pain. Note:	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic form directly from WIPO at	
CC	ftp.wipo.int/pub/published pct sequences.	

Query Match

Query Match	
Best Local Similarity	Score 2283; DB %;
Best Local Similarity	Prod No 5 90-150

Best Local Similarity 100.0%; Pred. No. 5.8e-158;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Cons 0.

QY	1	MASVVLPGSQC	CAAAAAA	APPGELRL	LLLLL	FSAAAL	PTG	DG	GNL	FTK	DV	VI	EG	VA	60
Db	1	MASVVLPGSQC	CAAAAAA	APPGELRL	LLLLL	FSAAAL	PTG	DG	GNL	FTK	DV	VI	EG	VA	60
QY	61	TIS	CCWNKSD	SDS	VI	QLLN	PN	QT	Y	IF	R	P	L	K	12
Db	61	TIS	CCWNKSD	SDS	VI	QLLN	PN	QT	Y	IF	R	P	L	K	12
QY	121	RYFC	Q	LY	T	D	P	P	Q	E	S	T	T	I	18
Db	121	RYFC	Q	LY	T	D	P	P	Q	E	S	T	T	I	18
QY	181	K	N	T	E	L	K	G	K	S	E	V	E	E	24
Db	181	K	N	T	E	L	K	G	K	S	E	V	E	E	24
QY	241	Y	K	P	Q	V	H	I	Q	M	T	Y	P	L	30

QY 1 MASVLPSSGQCAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
DB 1 MASVLPSSGQCAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
QY 61 TISQVNSKSDSVIQLLNPRTIYFRDPRPKDSRFQLLNPFSSSELKVSILTNVISDEG 120
DB 61 TISQVNSKSDSVIQLLNPRTIYFRDPRPKDSRFQLLNPFSSSELKVSILTNVISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEIEVNCVTAMASKPATIRWF 180
DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEIEVNCVTAMASKPATIRWF 180
QY 181 KGNTLKGKSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
DB 181 KGNTLKGKSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360
DB 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMCLLIILGRYFARHKGTYFTHAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMCLLIILGRYFARHKGTYFTHAKGADDAADA 420
QY 421 DTALINAEAGGQNNSEKKEYFI 442
DB 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 4
AAE19887
ID AAE19887 standard; protein; 442 AA.
XX
AC AAE19887;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
XX
KW Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200214557-A1.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025690.
XX
PR 15-AUG-2000; 2000US-0225264P.
XX
PA (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Reeves RH, Yoshinozi M;
XX
DR WPI; 2002-241913/29.
XX
PT Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC1) in subject, comprises contacting proliferating cell
PT of subject with reagent detecting TSLC1 and detecting modification in
PT TSLC1 level.
XX
PS Disclosure; Page 49-50; 59pp; English.
XX
CC The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a

CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1
XX
SQ Sequence 442 AA;
Query Match 100.0%; Score 2283; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.8e-158;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVLPSSGQCAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
DB 1 MASVLPSSGQCAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
QY 61 TISQVNSKSDSVIQLLNPRTIYFRDPRPKDSRFQLLNPFSSSELKVSILTNVISDEG 120
DB 61 TISQVNSKSDSVIQLLNPRTIYFRDPRPKDSRFQLLNPFSSSELKVSILTNVISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEIEVNCVTAMASKPATIRWF 180
DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEIEVNCVTAMASKPATIRWF 180
QY 181 KGNTLKGKSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
DB 181 KGNTLKGKSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360
DB 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMCLLIILGRYFARHKGTYFTHAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMCLLIILGRYFARHKGTYFTHAKGADDAADA 420
QY 421 DTALINAEAGGQNNSEKKEYFI 442
DB 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 5
ABP62825
ID ABP62825 standard; protein; 442 AA.
XX
AC ABP62825;
XX
DT 14-OCT-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 262.
XX
KW Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
KW burn; central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; immune disorder;
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
OS Homo sapiens.
XX
PN WO2002:8424-A2.

Claim 1; Page 81-82; 97pp; English.

PS The present sequence is a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
 CC Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from
 CC RNA isolated from lung tissue. A number of Incyte Clones were used to
 CC assemble the consensus sequence. BLAST analysis showed that the sequence
 CC is homologous to immuno-superfamily protein B12 g3779242. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HCSR may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR
 CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds

SQ Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 3; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGQCAAAAAAPPGLRLRLLLLSAALIFTDGQNLFTKDVTVIEGEVA 60

Db 1 MASVLPSSGQCAAAAAAPPGLRLRLLLLSAALIFTDGQNLFTKDVTVIEGEVA 60

QY 61 TISQVKNKSDSVTLQNLNPNRTIYFRDLKDRFQLNFSSELKVSILTNVISDEG 120

Db 61 TISQVKNKSDSVTLQNLNPNRTIYFRDLKDRFQLNFSSELKVSILTNVISDEG 120

QY 121 RYFCQLYTDPQPSYTTITVLVPPRNLMIDIKDTAVEGEIEVNCVTAMASKPATITIRWF 180

Db 121 RYFCQLYTDPQPSYTTITVLVPPRNLMIDIKDTAVEGEIEVNCVTAMASKPATITIRWF 180

QY 181 KGNTLKGKSEVESEWSMTVTTSQMLKVHKEDDGPVICOVEHPAVTGNLQTRYLEVQ 240

Db 181 KGNTLKGKSEVESEWSMTVTTSQMLKVHKEDDGPVICOVEHPAVTGNLQTRYLEVQ 240

QY 241 YKQVHIQMTYPLQGLTREGDALETCAIGKQPMVTVWVRVDDEMPQHAVLSGNLFI 300

Db 241 YKQVHIQMTYPLQGLTREGDALETCAIGKQPMVTVWVRVDDEMPQHAVLSGNLFI 300

QY 301 NNLKNTDNGTYRCEASNIVGKASHDYMVYVDPPTTIPPTTTTTTTTTTTTTTTTTITD 360

Db 301 NNLKNTDNGTYRCEASNIVGKASHDYMVYVDPPTTIPPTTTTTTTTTTTTTTTTTITD 360

QY 361 SRAGEGSTRADVHVGTVGVVAVVVFAMLCILILGRYPARHKGTYPTHEAKGADDAADA 420

Db 361 SRAGEGSTRADVHVGTVGVVAVVVFAMLCILILGRYPARHKGTYPTHEAKGADDAADA 420

QY 421 DTAINAEGGQNNSEKKEYFI 442

Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 3

AAV45092

ID AAY45092 standard; protein; 442 AA.

XX AC AAY45092;

XX DT 31-MAY-2000 (first entry)

XX Human lymphoid derived dendritic cell adhesion molecule.

XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;

KW B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;

XX

KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1. .374
 FT /label= Extracellular_domain
 FT Peptide 1. .38
 FT Protein 39. .442
 FT /label= Mature_human_LDCAM_polypeptide
 FT Modified-site 67. .69
 FT /note= "N-Glycosylation site"
 FT Modified-site 101. .103
 FT /note= "N-Glycosylation site"
 FT Modified-site 113. .115
 FT /note= "N-Glycosylation site"
 FT Modified-site 165. .167
 FT /note= "N-Glycosylation site"
 FT Modified-site 304. .306
 FT /note= "N-Glycosylation site"
 FT Modified-site 308. .310
 FT /note= "N-Glycosylation site"
 FT Domain 375. .395
 FT /label= Transmembrane_domain
 FT Domain 396. .442
 FT /label= Cytoplasmic_domain

PN W0200008158-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99MO-US017905.

XX 07-AUG-1998; 98US-0095672P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC;

XX WPI; 2000-205712/18.

XX N-PSDB; AA250882.

XX Novel molecules designated LDCAM are capable of altering or modulating T cell function.

XX Claim 7; Page 42-43; 44pp; English.

XX The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-L1. Human LDCAM is expressed in breast, retina, foetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7-L1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7-L1

XX Sequence 442 AA;

XX Query Match

XX Best Local Similarity 100.0%;

XX Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Score 2283; DB 3; Length 442;

XX Pred. No. 5.8e-158;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 50.5888 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title: US-09-778-187B-2
Perfect score: 2283
Sequence: 1 MASVVLPSGSCRAAAAAA.....ALINAGGQNNSEKKEFYI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2283	100.0	442	3 AAB25619	Protein e
2	2283	100.0	442	3 AAY94341	Human cel
3	2283	100.0	442	3 AAY45092	Human lym
4	2283	100.0	442	5 AAE19887	Human tum
5	2283	100.0	442	5 ABP62825	Human pol
6	2283	100.0	442	6 ADA27144	Human nov
7	2283	100.0	442	7 ADE54238	Human pro
8	2283	100.0	442	8 ADE86685	Human hum
9	2280	99.9	442	6 ABO07196	Novel hum
10	2280	99.9	442	6 ABO07231	Human p53
11	2280	99.9	442	7 ADE61605	Human pro
12	2280	99.9	442	7 ADE61608	Human pro
13	2263	99.1	440	2 AAY17830	Human pro
14	2263	99.1	440	3 AAB01321	Human pro
15	2263	99.1	440	4 AAU29040	Human pro
16	2263	99.1	440	6 ABUS8416	Human pro
17	2263	99.1	440	6 ABUS7964	Human pro
18	2263	99.1	440	6 ABUS7964	Novel hum
19	2263	99.1	440	6 ABR66153	Human sec
20	2263	99.1	440	6 ABR65543	Human sec
21	2263	99.1	440	6 ABUS9483	Human sec
22	2263	99.1	440	6 ABUS5930	Human sec
23	2263	99.1	440	6 ABUS2722	Human pro
24	2263	99.1	440	6 ABUS9843	Novel hum
25	2263	99.1	440	6 ABR68092	Human sec

ALIGNMENTS

RESULT 1
AAB25619
ID AAB25619 standard; protein; 442 AA.
XX AC AAB25619;
XX AC AAB25619;
DT 21-NOV-2000 (first entry)
XX XX
DE Protein encoded by human secreted protein gene #11.
XX XX
KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antineumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnery; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.
XX OS Homo sapiens.
XX XX
PN WO200029435-A1.
XX XX
PD 25-MAY-2000.
XX XX
PF 27-OCT-1999; 99WO-US025031.
XX XX
PR 28-OCT-1998; 98US-0105971P.
XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
PI Greene JM;
XX XX
WPI; 2000-387742/33.
XX XX
PT Isolated nucleic acid molecules encoding human secreted proteins are used
PT for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases.
XX XX
PS Disclosure; Page 182-183; 803pp; English.
XX XX
CC The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given in
CC AAA80606-A80623 encode the 12 secreted protein sequences given in
CC AAB25576-B25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the

Abu96145 Novel hum
Abu92576 Human sec
Abc08653 Human sec
Abc02705 Human sec
Abr74859 Human sec
Abu94621 Human sec
Abu60240 Human PRO
Abu85594 Human PRO
Abu98754 Novel hum
Abu97969 Novel hum
Abu91675 Novel hum
Abu89368 Human PRO
Abu86209 Human sec
Abu67422 Human sec
Abu80450 Human PRO
Abu84508 Human PRO
Abu93658 Human sec
Abr98758 Human sec
Abol6281 Human sec
Abr92181 Human sec
Abol8822 Human sec

2263 99.1 440 6 ABU96145
2263 99.1 440 6 ABU92576
2263 99.1 440 6 ABO08653
2263 99.1 440 6 ABO02705
2263 99.1 440 6 ABR74859
2263 99.1 440 6 ABR94621
2263 99.1 440 6 ABU60240
2263 99.1 440 6 ABU85594
2263 99.1 440 6 ABU98754
2263 99.1 440 6 ABU97969
2263 99.1 440 6 ABU91675
2263 99.1 440 6 ABU89368
2263 99.1 440 6 ABU86209
2263 99.1 440 6 ABU67422
2263 99.1 440 6 ABU80450
2263 99.1 440 6 ABR93658
2263 99.1 440 6 ABR98758
2263 99.1 440 6 ABO16281
2263 99.1 440 6 ABR92181
2263 99.1 440 6 ABO18822

```
Db 61 KVHKEDDGPVVCQVEHFAVNTGLQRYLEQYKPVQVHIQMTYPLQGLTREGDALELTC 120
QY 268 EAIGKPPQPMVTVWVDDMPHAYLSPGNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
Db 121 EAIGKPPQPMVTVWVDDMPHAYLSPGNLFINNLTNDNGTYRCEASNIVGKAHSDYI 180
QY 328 LYVYDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 387
Db 181 LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDHAVIGGVAVVVFA 223
QY 388 MCLLLIILGRYFARHKGTYFTHAKGADDAADATTAIINAEQQNNSEEKEYFI 442
Db 224 MCLLLIILGRYFARHKGTYFTHAKGADDAADATTAIINAEQQNNSEEKEYFI 278
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RESULT 15

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Q8N3J6 PRELIMINARY; PRT; 435 AA.
AC Q8N3J6;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP761G128
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgama;
EA Koshner K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG_3.
DR SMART; SMO0409; IG; 2.
DR SMART; SMO0408; IGC2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;
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Query Match 39.6%; Score 903; DB 4; Length 435;
Best Local Similarity 44.4%; Pred. No. 1.le-68;
Matches 193; Conservative 76; Mismatches 138; Indels 28; Gaps 7;
QY 29 LLLFSAALIPG-DGQNLFTKDVTVIEGVATISQVKNKSDSVIQLLNPNRQTIYFR 87
Db 8 VLRYSYVGLLQSQGQFPPLQNTVVVEGTAITLCRDQNDNTSLQWNPAAQTLTFD 67
QY 88 DFRPLKDSRFQLNFSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTITVLVPPRL 147
Db 68 DKKALRDNRIELVRASWHELSISVDSVLSDEGQYTCSLFTMPVKTSKAVITLVGVPEK 127
QY 148 MIDIQKTAVEGEIEFVNCATAMASKPATTTIRWFKGNTLKGKSEVEWS---DMYVTVSQ 204
Db 128 QISGFSPVMEGLMQLTKCTSGSKPAADIRWFKNDKEIKDKVYLKEEDANRKTFTVSST 187
QY 205 LMLKVHKEDDGPVVCQVEHFAVNTGLQRYLEQYKPVQVHIQMTYPLQGLTREGDAL 263
Db 188 LDFRVDSDDGVAVICRVHESLNATQVAMQVLEIHIYTPSVKI---IPSTPPQEQPL 244
QY 264 ELTCEAJGKPPQPMVTVWVDDEN--PQHAVLSGNLFINNLTNDNGTYRCEASNIVGK 321
Db 245 ILTCESKGPLPEPVLWTKDGGELPDPDRVWVSGRELNLFLNKTNDNGTYRCEATNIQ 304
QY 322 AHSYMLYVYDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 367
Db 305 SSAEYVLIVHDPNTLLFTIIPSLTTATVTVAITTSPTTSATTSSIRDPNALAGQNG 364
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QY 358 SIRAVDHAVIGGVAVVVVFAVLCILIIILGRYFARHKGTYFTHAKGADDAADATTAIIN 427
Db 355 P----DHALIGGI VAVVVVFTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIIN 420
QY 428 EGGQNNSEEKEYFI 442
Db 421 EGSQVNAEKEYFI 435
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Search completed: May 27, 2004, 09:34:55
Job time : 39.2466 secs

DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;

Query Match 65.0%; Score 1483; DB 11; Length 295;
 Best Local Similarity 95.9%; Pred. No. 1.4e-118;
 Matches 283; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 148 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQORYLEVQVKPQVHIQMTYPLQGLTREGDALELTC 267
 Db 61 KVHKEDDGPVICOVEHPAVTGNLQORYLEVQVKPQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIKGPQPMVTWVRVDDMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
 Db 121 EAIKGPQPMVTWVRVDDMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 180
 QY 328 LYVDDPTTTPPPPTTT 387
 Db 181 LYVDDPTTTPPPPTTT 240
 QY 388 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKKEYFI 442
 Db 241 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKKEYFI 295

RESULT 13
 QYQYL5
 ID QYQYL5 PRELIMINARY; PRT; 289 AA.
 AC QYQYL5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175B.
 GN IGSF4 OR RAI175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565ABA4 CRC64;

Query Match 61.1%; Score 1394; DB 11; Length 289;
 Best Local Similarity 91.9%; Pred. No. 5.6e-111;
 Matches 271; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

QY 148 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQORYLEVQVKPQVHIQMTYPLQGLTREGDALELTC 267
 Db 61 KVHKEDDGPVICOVEHPAVTGNLQORYLEVQVKPQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIKGPQPMVTWVRVDDMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
 Db 121 EAIKGPQPMVTWVRVDDMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 180
 QY 328 LYVDDPTTTPPPPTTT 387
 Db 181 LYVDDPTTTPPPPTTT 234
 QY 388 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKKEYFI 442
 Db 235 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKKEYFI 289

RESULT 14
 QYQYL3
 ID QYQYL3 PRELIMINARY; PRT; 278 AA.
 AC QYQYL3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175N.
 GN IGSF4 OR RAI175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021967; BAA87917.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

Query Match 60.0%; Score 1370.5; DB 11; Length 278;
 Best Local Similarity 90.2%; Pred. No. 5.4e-109;
 Matches 266; Conservative 3; Mismatches 9; Indels 17; Gaps 1;

QY 148 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQORYLEVQVKPQVHIQMTYPLQGLTREGDALELTC 267

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN IGSF4 OR NEC12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunosuperfamily.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061260; AAC67243.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488 CRC64;
 Query Match 66.8%; Score 1526; DB 11; Length 295;
 Best Local Similarity 98.6%; Pred. No. 2.9e-122;
 Matches 291; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 148 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFGKNTLKGKSEVEWSDMYTTSQML 207
 DB 1 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFGKNTLKGKSEVEWSDMYTTSQML 60
 QY 208 KVHEDDGVPIQVQVHPAVTGNLTQRYLEVQKPVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KVHEDDGVPIQVQVHPAVTGNLTQRYLEVQKPVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFINLNKTDNGTYRCEASNVGKAHSDYM 327
 DB 121 EAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFINLNKTDNGTYRCEASNVGKAHSDYM 180
 QY 328 LVYVDPPTTTPPTTT 387
 DB 181 LVYVDPPTTTPPTTT 240
 QY 388 MLCLLIIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNSEEKKEYFI 442
 DB 241 MLCLLIIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNSEEKKEYFI 295
 RESULT 11
 Q9QYL4
 ID Q9QYL4 PRELIMINARY; PRT; 306 AA.
 AC Q9QYL4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175C.
 GN IGSF4 OR RAI175C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021964; BAA87914.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.

RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021966; BAA87916.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
 Query Match 65.9%; Score 1503.5; DB 11; Length 306;
 Best Local Similarity 94.8%; Pred. No. 2.5e-120;
 Matches 290; Conservative 2; Mismatches 3; Indels 11; Gaps 1;
 QY 148 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFGKNTLKGKSEVEWSDMYTTSQML 207
 DB 1 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFGKNTLKGKSEVEWSDMYTTSQML 60
 QY 208 KVHEDDGVPIQVQVHPAVTGNLTQRYLEVQKPVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KVHEDDGVPIQVQVHPAVTGNLTQRYLEVQKPVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFINLNKTDNGTYRCEASNVGKAHSDYM 327
 DB 121 EAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFINLNKTDNGTYRCEASNVGKAHSDYM 180
 QY 328 LVYVDPPTTTPPTTT 376
 DB 181 LVYVDPPTTTPPTTT 240
 QY 377 IGVVAVVFPFAMCLLIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNSEE 436
 DB 241 IGVVAVVFPFAMCLLIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNSEE 300
 QY 437 KKEYFI 442
 DB 301 KKEYFI 306
 RESULT 12
 Q9QYL6
 ID Q9QYL6 PRELIMINARY; PRT; 295 AA.
 AC Q9QYL6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175A.
 GN IGSF4 OR RAI175A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021964; BAA87914.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.

RP	SEQUENCE FROM N.A.					
RC	STRAIN=CSYBL/6U; TISSUE=Hippocampus;					
RX	MEDLINE=C57BL/6J; PubMed=11217851;					
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
RA	Akaiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,					
RA	Aizawa K., Izawa M., Nishi K., Kiyoawa H., Kondo S., Yamataka I.,					
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,					
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,					
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,					
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,					
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,					
RA	Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,					
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,					
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,					
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,					
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,					
RA	Nordone P., Ring B., Bingwald M., Rodriguez I., Sakamoto N.,					
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,					
RA	Suzuki H., Ioyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,					
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,					
RA	Hayashizaki Y.;					
RT	"Functional annotation of a full-length mouse cDNA collection.";					
RL	Nature 409:685-690(2001).					
DR	EMBL: AK013775; BAB28988.1; -;					
DR	MGI: 1889272; IGsf4.					
DR	GO: GO:0045202; C:synaptic junction; IDA.					
DR	GO: GO:008021; C:synaptic vesicle; IDA.					
DR	GO: GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.					
DR	GO: GO:0005515; F:protein binding; IPI.					
DR	GO: GO:0007155; P:cell adhesion; IDA.					
DR	GO: GO:0007416; P:synaptogenesis; IDA.					
DR	InterPro: IPR007110; Ig-like.					
DR	InterPro: IPR003598; Ig_c2.					
DR	Pfam: PF00047; Ig; 3.					
DR	SMART: SM00408; IGC2; 1.					
DR	PROSITE; PS00835; IG_LIKE; 3.					
KX	Immunoglobulin domain.					
SQ	SEQUENCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;					
Query Match 73.2%; Score 1671.5; DB 11; Length 336;						
Best Local Similarity 97.3%; Pred. No. 1.2e-134;						
Matches 325; Conservative 0; Mismatches 6; Indels 3; Gaps						
Qy	1 MASVILPSGSQCAAA---AAAAAPGLRLRLLLLFSAALIPTDGNGNLTQKVTVEG	57				
Dd	1 MASAVLDGSGCAAAAATAAAPGLRLRLULLLSAALIPDGGQLLFTKVTVTEG	60				
Qy	58 EVATTSCQNKSDSVIQLLNPNRQTIVFRPRLKDSRFOLLFSSELKVSILTNSVIS	111				
Dd	61 EVAT-SCQNKSDSVIQLLNPNRQTIVFRPRLKDSRFOLLFSSELKVSILTNSVIS	120				
Qy	118 DEGRFYCOLYTPDPESYTITLVLPPLNMIDIKDTAVEGEIEINCTAMAKSPATTI	177				
Dd	121 DEGRFYCOLYTPDPESYTITLVLPPLNMIDIKDTAVEGEIEINCTAMAKSPATTI	180				
Qy	178 RWFKNTELKGKSEVEEWSDMYTVTSQLMKVKHEDDGVPVICOVEHPANTGNLTORYL	233				
Dd	181 RWFKNTELKGKSEVEEWSDMYTVTSQLMKVKHEDDGVPVICOVEHPANTGNLTORYL	240				
Qy	238 EVOYKPQVHIOMTYPLOGLTREGDALELTCEAIKGPQVMVTVRVVDDEMQHAVLSGPN	297				
Dd	241 EVOYKPQVHIOMTYPLOGLTREGDAFELTCEAIKGPQVMVTVRVVDDEMQHAVLSGPN	300				
Qy	298 LFNNLNKTNDGTNRCEASNTVGKAHDYMLYYV 331					
Dd	301 LFNNLNKTNDGTNRCEASNTVGKAHDYMLYYV 334					
RESULT 10						
Q92ZH8						
ID Q92ZH8	PRELIMINARY;	PRT;	295 AA.			
AC Q92ZH8;						
DT 01-MAY-1999 (TrEMBLrel. 10, Created)						


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Db 121 TISCQVNSDDSVIQLLNPNRTIYFRDPLKDSRQFLLNFSSELKVSLSNVSISDEG 120
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Db 121 RYFCOLYTDPPQESYTIIVLPPNLMIDIOKDTAVEGEEIEVNCETAMASKPATIRWF 180
QY 181 KGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
Db 181 KGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTT-LTIIT 359
Db 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTT-LTIIT 359
QY 360 DSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAAD 419
Db 361 DSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAAD 420
QY 420 ADTAIINAEQGNNSSEKKEYFI 442
Db 421 ADTAIINAEQGNNSSEKKEYFI 443

RESULT 6
Q7TNL1 PRELIMINARY; PRT; 417 AA.
AC Q7TNL1;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE Nectin-like molecule 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Shingai T., Ikeda W., Kakuwaga S., Morimoto K., Takekuni K., Itoh S.,
RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
RT "Implications of nectin-like molecule
RT 2/IGSF4/RA175/SgIGSF/TS1C1/SynCAM1 in cell-cell adhesion and
RT transmembrane protein localization in epithelial cells.";
RL J. Biol. Chem. 0:0-0(2003).
DR EMBL; AY351388; AAQ02381.1; -
SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

Query Match 90.7%; Score 2071.5; DB 11; Length 417;
Best Local Similarity 91.7%; Pred. No. 9.2e-169;
Matches 408; Conservative 1; Mismatches 5; Indels 31; Gaps 2;

QY 1 MASVLPSSGSCAAA---AAAAAPGLRLRLRLRLRLRLLSAALIPFGDGNLFTKDVTVIEG 57
Db 1 MASVLPSSGSCAAA---AAAAAPGLRLRLRLRLRLRLLSAALIPFGDGNLFTKDVTVIEG 60
QY 58 EVATISQVNSDDSVIQLLNPNRTIYFRDPLKDSRQFLLNFSSELKVSLSNVSIS 117
Db 61 EVATISQVNSDDSVIQLLNPNRTIYFRDPLKDSRQFLLNFSSELKVSLSNVSIS 120
QY 118 DEGRYFCOLYTDPPQESYTIIVLPPNLMIDIOKDTAVEGEEIEVNCETAMASKPATI 177
Db 121 DEGRYFCOLYTDPPQESYTIIVLPPNLMIDIOKDTAVEGEEIEVNCETAMASKPATI 180
QY 178 RWFKGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYL 237
Db 181 RWFKGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYL 240
QY 238 EVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGN 297
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Db 241 EVQYKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGN 300
QY 298 LFINLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTI 357
Db 301 LFINLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTTTTTI 357
QY 358 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDA 417
Db 335 --DSRAGEEGTIGAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDA 392
QY 418 ADATAIINAEQGNNSSEKKEYFI 442
Db 393 ADATAIINAEQGNNSSEKKEYFI 417

RESULT 7
Q86WB8 PRELIMINARY; PRT; 333 AA.
AC Q86WB8;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Secretary isoform of TS1C-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SgIGSF/TS1C-1.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094146; BAC66178.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; Igc2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;

Query Match 75.1%; Score 1715; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.2e-138;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAA---AAAAAPGLRLRLRLRLRLLSAALIPFGDGNLFTKDVTVIEG 60
Db 1 MASVLPSSGSCAAA---AAAAAPGLRLRLRLRLRLLSAALIPFGDGNLFTKDVTVIEG 60
QY 61 TISCQVNSDDSVIQLLNPNRTIYFRDPLKDSRQFLLNFSSELKVSLSNVSISDEG 120
Db 61 TISCQVNSDDSVIQLLNPNRTIYFRDPLKDSRQFLLNFSSELKVSLSNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTIIVLPPNLMIDIOKDTAVEGEEIEVNCETAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTIIVLPPNLMIDIOKDTAVEGEEIEVNCETAMASKPATIRWF 180
QY 181 KGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
Db 181 KGNTELKGSKEVEESDMYTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLTQRYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVY 331
Db 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVY 331
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Db 1 MASVLPSCGQCAAAAVAAAAAPGLRLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
QY 58 EVATISCCQVNSKSDSVIQLLNPNTQTIYFRDPLKDSRFQLLNFSSSELKVSLLTNVSI 117
Db 61 EVATISCCQVNSKSDSVIQLLNPNTQTIYFRDPLKDSRFQLLNFSSSELKVSLLTNVSI 120
QY 118 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCTAMASKPATI 177
Db 121 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCTAMASKPATI 180
QY 178 RWFKNTELKSGSEVEESDMYTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLTQRYL 237
Db 181 RWFKNTELKSGSEVEESDMYTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLTQRYL 240
QY 238 EVQKPVQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDMPQHAVLSGN 297
Db 241 EVQKPVQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDMPQHAVLSGN 300
QY 298 LFINNLKNDNGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTI 357
Db 301 LFINNLKNDNGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTI 360
QY 358 ITDSRAGEGSTRADVHAGVAVVAVFAMLCILILGRYFARHKGTYFTHAKGADDA 417
Db 361 ITDSRAGEGSTRADVHAGVAVVAVFAMLCILILGRYFARHKGTYFTHAKGADDA 420
QY 418 ADADTAIINAEQQNNSEKKEYFI 442
Db 421 ADADTAIINAEQQNNSEKKEYFI 445

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RESULT 4

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Q8R5M8 ID Q8R5M8 PRELIMINARY; PRT; 456 AA.
AC Q8R5M8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RA175.
GN IGSF4 OR RA175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Momoi T.;
RT "Biological function of RA175, a new member of immunoglobulin super
family."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064265; BAB83501.2; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 45787 MW; 3226E866A4BC1C7F CRC64;

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Query Match 97.3%; Score 2221; DB 11; Length 456;
 Best Local Similarity 95.4%; Pred. No. 1.7e-181;
 Matches 435; Conservative 2; Mismatches 5; Indels 14; Gaps 2;

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QY 1 MASVLPSCGQCAAA--AAAAAPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 57
Db 1 MASVLPSCGQCAAAAVAAAAAPGLRLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
QY 58 EVATISCCQVNSKSDSVIQLLNPNTQTIYFRDPLKDSRFQLLNFSSSELKVSLLTNVSI 117
Db 61 EVATISCCQVNSKSDSVIQLLNPNTQTIYFRDPLKDSRFQLLNFSSSELKVSLLTNVSI 120
QY 118 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCTAMASKPATI 177
Db 121 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCTAMASKPATI 180
QY 178 RWFKNTELKSGSEVEESDMYTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLTQRYL 237
Db 181 RWFKNTELKSGSEVEESDMYTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLTQRYL 240
QY 238 EVQKPVQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDMPQHAVLSGN 297
Db 241 EVQKPVQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVWVTVRVDDMPQHAVLSGN 300
QY 298 LFINNLKNDNGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTI 357
Db 301 LFINNLKNDNGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTI 360
QY 358 IT-----DSRAGEGSTRADVHAGVAVVAVFAMLCILILGRYFARHKGTY 406
Db 361 ITDTATTEPAVHDSRAGEGTRIGAVDHAGVAVVAVFAMLCILILGRYFARHKGTY 420
QY 407 FTHEAKGADDAADATTAIINAEQQNNSEKKEYFI 442
Db 421 FTHEAKGADDAADATTAIINAEQQNNSEKKEYFI 456

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RESULT 5

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Q8N2F4 ID Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC Q8N2F4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagabari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BAC11657.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

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Query Match 93.5%; Score 2134.5; DB 4; Length 443;
 Best Local Similarity 94.4%; Pred. No. 4.1e-174;
 Matches 418; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

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QY 1 MASVLPSCGQCAAAAPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEGVA 60
Db 1 MASVLPSCGQCAAAAPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEGVA 60
QY 61 TISCCQVNSKSDSVIQLLNPNTQTIYFRDPLKDSRFQLLNFSSSELKVSLLTNVSI 120

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QY 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSELKVSILTNVSI 120
 DB 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSELKVSILTNVSI 120
 QY 121 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEEIEVNCCTAMASKPATTIRWF 180
 DB 121 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEEIEVNCCTAMASKPATTIRWF 180
 QY 181 KGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYLEVQ 240
 DB 181 KGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYLEVQ 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDEMPQHAVLSGPNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDEMPQHAVLSGPNLFI 300
 QY 301 NNLNKTNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTITD 360
 DB 301 NNLNKTNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTITD 360
 QY 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 DB 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 QY 421 DTALINAEAGGQNNSEKKEYFI 442
 DB 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 2

Q8R41L ID Q8R41L PRELIMINARY; PRT; 445 AA.
 AC Q8R41L;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor suppressor in lung cancer 1.
 GN IGSF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RA Fukami T., Maruyama T., Murakami Y.;
 RT "Identification of murine orthologue of the TSLC1 gene."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF434663; AAL86736.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003598; Neurexin-like.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;

Query Match 98.2%; Score 2241.5; DB 11; Length 445;
 Best Local Similarity 98.0%; Pred. No. 2.8e-183;
 Matches 436; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 1 MASVVLPSGSCQAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 57
 DB 1 MASVVLPSGSCQAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 57

QY 58 EVATISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSELKVSILTNVSI 117
 DB 61 EVATISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSELKVSILTNVSI 120
 QY 1-8 DEGRYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEEIEVNCCTAMASKPATTI 177
 DB 121 DEGRYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEEIEVNCCTAMASKPATTI 180
 QY 178 RWFKGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 237
 DB 181 RWFKGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 240
 QY 238 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDEMPQHAVLSGPN 297
 DB 241 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDEMPQHAVLSGPN 300
 QY 298 LFNNLNKTNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTIT 357
 DB 301 LFNNLNKTNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTIT 360
 QY 358 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 417
 DB 361 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 QY 418 ADADTAIINAEAGGQNNSEKKEYFI 442
 DB 421 ADADTAIINAEAGGQNNSEKKEYFI 445

RESULT 3

Q8K3T6 ID Q8K3T6 PRELIMINARY; PRT; 445 AA.
 AC Q8K3T6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Synaptic cell adhesion molecule 1.
 GN IGSF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Biederer T., Sara Y., Moshayeva M., Atasoy D., Liu X., Kavalali E.T.,
 RA Sudhof T.C.;
 RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly."
 RL Science 0:0-0(2002).
 DR EMBL; AF539424; AAN01614.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IGC2; 3.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 97.8%; Score 2232.5; DB 11; Length 445;
 Best Local Similarity 97.5%; Pred. No. 1.7e-182;
 Matches 434; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 1 MASVVLPSGSCQAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 57

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 36.2466 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-2

Perfect score: 283

Sequence: 1 MASVLPSSGSCACAAAAA.....AIIAEGSQNNSEKKEYFI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2280	99.9	442	Q9BY67	Q9by67 homo sapien
2	2241.5	98.2	445	Q8R4L1	Q8r4l1 mus musculus
3	2232.5	97.8	445	Q8K3T6	Q8k3t6 mus musculus
4	2221	97.3	456	Q8R5M8	Q8r5m8 mus musculus
5	2134.5	93.5	443	Q8N2F4	Q8n2f4 homo sapien
6	2071.5	90.7	417	Q7TNL1	Q7tnl1 mus musculus
7	1715	75.1	333	Q86WB8	Q86wb8 homo sapien
8	1683.5	73.7	336	Q8OVG4	Q8ovg4 mus musculus
9	1671.5	73.2	336	Q9D6E7	Q9d6e7 mus musculus
10	1526	66.8	295	Q922H8	Q92zh8 mus musculus
11	1503.5	65.9	306	Q9QYL4	Q9qyl4 mus musculus
12	1483	65.0	285	Q9QYL6	Q9qyl6 mus musculus
13	1394	61.1	289	Q9QYL5	Q9qyl5 mus musculus
14	1370.5	60.0	278	Q9QYL3	Q9qyl3 mus musculus
15	903	39.6	435	Q8N3J6	Q8n3j6 homo sapien
16	893	39.1	437	Q8I2P8	Q8i2p8 homo sapien

17	863	37.8	395	11	Q8BXJ7	Q8bxj7 mus musculus
18	862.5	37.8	404	11	Q8BLQ9	Q8blq9 mus musculus
19	860	37.7	395	11	Q8BZP4	Q8bzp4 mus musculus
20	858.5	37.6	404	11	Q8BYP1	Q8byp1 mus musculus
21	802	35.1	394	13	Q7ZXX1	Q7zxx1 xenopus lae
22	767	33.6	388	4	Q8NFZ8	Q8niz8 homo sapien
23	758	33.2	388	11	Q8R464	Q8r464 mus musculus
24	744.5	32.6	396	11	Q9NM28	Q9nm28 mus musculus
25	739	32.4	398	4	Q8N126	Q8n126 homo sapien
26	732.5	32.1	381	4	Q9Y4A4	Q9y4a4 homo sapien
27	722	31.6	432	4	Q9UJL1	Q9ujl1 homo sapien
28	379.5	16.6	163	11	Q8KIH8	Q8kih8 mus musculus
29	370.5	16.2	163	4	Q9NVJ5	Q9nvj5 homo sapien
30	368.5	16.1	152	11	Q8BSQ8	Q8bsq8 mus musculus
31	341.5	15.0	549	11	Q9D006	Q9d006 mus musculus
32	338.5	14.8	549	11	Q9JLB9	Q9jlb9 mus musculus
33	335.5	14.7	549	4	Q9NQS3	Q9nqs3 homo sapien
34	325.5	14.3	234	4	Q8IZO9	Q8izq9 homo sapien
35	315.5	13.9	438	11	Q9JLB7	Q9jlb7 mus musculus
36	315.5	13.9	510	11	Q9JLB8	Q9jlb8 mus musculus
37	287	12.6	439	13	Q57349	Q57349 gallus gall
38	268	11.7	407	4	Q9Y4I2	Q9y4i2 homo sapien
39	265	11.6	1482	5	Q9V4Y0	Q9v4y0 drosophila
40	263.5	11.5	5175	5	Q8I0L3	Q8i0l3 caenorhabdi
41	261.5	11.5	5198	5	Q765I8	Q765i8 caenorhabdi
42	261.5	11.5	510	4	Q96N18	Q96ny8 homo sapien
43	261.5	11.5	510	4	Q96K15	Q96kis homo sapien
44	254.5	11.1	400	6	Q8HY16	Q8hy16 cebus apell
45	247.5	10.8	530	11	Q80XJ5	Q80xj5 mus musculus

ALIGNMENTS

RESULT 1

Q9BY67 Q9BY67 PRELIMINARY; PRT; 442 AA.
AC Q9BY67;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Nectin-like protein 2.
GN NECL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin superfamily.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132811; AAF69029.1; -.
DR Genew; HGNC:5951; IGSP4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurxin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 99.9%; Score 2280; DB 4; Length 442;
Best Local Similarity 99.8%; Pred No. 1.4e-186;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVLPSSGSCACAAAAAAPPGLRLRLLLLFSAALIPGTGGQNLFTKDVTVIEGEVA 60
DB 1 MASVLPSSGSCACAAAAAAPPGLRLRLLLLFSAALIPGTGGQNLFTKDVTVIEGEVA 60


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FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718 POTENTIAL.
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT CHAIN 21 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 594 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; C3D034106C5741C1 CRC64;

Query Match 9.7%; Score 222; DB 1; Length 837;
Best Local Similarity 24.1%; Pred. No. 2.6e-08;
Matches 120; Conservative 70; Mismatches 172; Indels 136; Gaps 28;

Qy 49 TKDVTVI-----EGETVISCQVNSKSDSVQILNPNRQTYPRDF 89
Db 102 TQETAVLEIYQKLTREWSQBFKQGDAAVVCVRSSPAPAVSWLYHNEEV-----155

Qy 90 RPLKDSFQLINSSSELKSLTWSIDEGRYFCOLYTDPPQ--SYTTIVL--VSPRN 146
Db 156 TTISDNLAML-----ANNLOILNINKSDGIYRCGEVARGIDPRDIIVNVNPPAI 211

Qy 147 LMIDIQKD---TAVEGEIEVNCATAMSKPATTIRWFKGNTLKGSEVBEWSDMYTV--201
Db 212 SM--POKSFNATABRGEMTFSCRASGS--PEPAISWFR-----NGKL-IEE-NEKYILKG 261

Qy 202 -TSQMLKVHKEDDGVPIQVEHPATGNLOTORYLEVQVQKPVHIOPTYLOGLTREG 260
Db 262 SNELTVRNINSDGGYVCRATNKA--GEDEKQAFQVFPQPHI--IQLK--NETTYEN 315

Qy 261 DALELTCEAIGKQPPVMVTVR--VD-----DMP-----QHAVLSGPNLFINNLN 304
Db 316 GQVTLVCDAGEPIP-BITWKRAVDGFTFTEGDKSPGRIEVKGQH---GSSSLHKDVK 371

Qy 305 KTDNGTYRCE-ASNIVGKAHSDYMLYVY-----DPPPTT 336
Db 372 LSGSGRYDCAASRIGGHQKSMYLDIEYAPKFIQNTIYYSWEGNPINISCDVKSNPPAS 431

Qy 337 I-----PPPTTTTTTTTTTTTTTTTTLITDSRAGEEG--SRAVDHAVIGGVAVVV 395
Db 432 IHWERDKVLPAKNTNLTYSYTGKRMILEIAPSDNDGFRYCNCTATNH--IGTRFQEIY 489

Qy 386 FAMLCL-----LIILGRYFAR-----HKGYTFYTHEAKGADDAADATTAI NAEG 429
Db 490 LALADVPSSPYGVKILIELSQTAKVSNKPNKPSDGHGVPDHHYQVDVKEVASEIKVIRSHG 549

Qy 430 GQ-----NNSEEKKEYFI 442
Db 550 VQTMVVLNNLEPNTTVEI 567

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RESULT 15

NPNH MOUSE

ID NPNH_MOUSE

AC Q9QZS7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DN Nephrin precursor (renal glomerulus-specific cell adhesion receptor).
GN NPHS1 OR NPHN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RX MEDLINE=99436348; PubMed=10504499;
RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holthofer H.,
RA Abrahamson D.R.;
RT "Nephrin localizes to the slit pore of the glomerular epithelial
cell.";
RL Kidney Int. 56:1481-1491(1999).
RN [2]
RP INTERACTION WITH CD2AP.
RP MEDLINE=21590051; PubMed=11733379;
RX Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
RA "CD2AP localizes to the slit diaphragm and binds to nephrin via a
novel C-terminal domain.";
RL Am. J. Pathol. 159:2303-2308(2001).
RN [3]
RP INTERACTION WITH CD2AP AND NPHS2.
RP MEDLINE=21590460; PubMed=11733557;
RX Schwarz K., Simons M., Reiser J., Saleem M.A., Faul C., Kriz W.,
RA Shaw A.S., Holzman L.B., Mundel P.;
RT "Podocin, a raft-associated component of the glomerular slit
diaphragm, interacts with CD2AP and nephrin.";
RL J. Clin. Invest. 108:1621-1629(2001).
CC -!- FUNCTION: Seems to play a role in the development or function of
the kidney glomerular filtration barrier. May anchor the podocyte
slit diaphragm to the actin cytoskeleton.
CC -!- SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
domain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
at podocyte slit diaphragm between podocyte foot processes.
CC -!- TISSUE SPECIFICITY: Expressed in kidney glomeruli.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 8 immunoglobulin-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
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or send an email to license@isb-sib.ch).
CC EMBL; AF168466; AAF03368.1; --
CC MGD; MGI:1859637; Nphs1.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007254; P:JNK cascade; IDA.
CC GO; GO:000165; P:MAPKK cascade; IDA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; IG-like.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00047; ig; 8.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS50835; IG_LIKE; 8.
KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Phosphorylation.
FT SIGNAL 1 22
FT CHAIN 23 1242 NEPHRIN.
FT DOMAIN 23 1064 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1065 1086 POTENTIAL.
FT DOMAIN 1087 1242 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 1330 IG-LIKE C2-TYPE 1.

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```
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 GPI-anchor amidated asparagine
FT LIPID (Potential).
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 321 NEUTROTRIMIN.
FT PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-anchor amidated asparagine
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE5B33B224 CRC64;

Query Match 10.1%; Score 230; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 2.2e-09;
Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;

QY 29 LLLLSAALIPFGDQGNLFK---DVTVEGEVATISQVKNKSDSDSVIQLLNPRTI- 84
Db 19 LRLLELVPTGVPRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAMLNRSSTIL 75

QY 85 YFRDFRPLKDSRFQLLNFSSSELKSLTVNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
Db 76 YAGNDKWCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVS 135

QY 144 PRNLMIDIKDTAV-EGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEESDMYTVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTVRHSIPKAVGFVSEDEYLEIQGIT 192

QY 203 SOLMLKVH---KEDDGVVPCVQHEPAVTGNLQTVRYLEVQVQKPOVHIQMTYPLQGL-TR 258
Db 193 REQSGDYECASNDVAAPVRRVK-----VTVNYPPYIS-----EAKGTGVP 234

QY 259 EGDALTELTCEALGKQPPVMVTVRVDDEMPQH-----AVLSGP---NLFINNKNKTNDNGTY 311
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNV 293

QY 312 RCEASNVGKAHSDYMLY 329
Db 294 TCVASNKLGHNTNASIMLF 311

RESULT 12
NCM2_MOUSE
ID NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
adhesion molecule) (R4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=3AUB/c; TISSUE=Olfactory neuroepithelium;
```

```
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 GPI-anchor amidated asparagine
FT LIPID (Potential).
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 321 NEUTROTRIMIN.
FT PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-anchor amidated asparagine
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE5B33B224 CRC64;

Query Match 10.1%; Score 230; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 2.2e-09;
Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;

QY 29 LLLLSAALIPFGDQGNLFK---DVTVEGEVATISQVKNKSDSDSVIQLLNPRTI- 84
Db 19 LRLLELVPTGVPRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAMLNRSSTIL 75

QY 85 YFRDFRPLKDSRFQLLNFSSSELKSLTVNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
Db 76 YAGNDKWCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVS 135

QY 144 PRNLMIDIKDTAV-EGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEESDMYTVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTVRHSIPKAVGFVSEDEYLEIQGIT 192

QY 203 SOLMLKVH---KEDDGVVPCVQHEPAVTGNLQTVRYLEVQVQKPOVHIQMTYPLQGL-TR 258
Db 193 REQSGDYECASNDVAAPVRRVK-----VTVNYPPYIS-----EAKGTGVP 234

QY 259 EGDALTELTCEALGKQPPVMVTVRVDDEMPQH-----HAVLSGNLFINNKNKTNDNG 309
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLRITFF--NVSEHDYG 291

QY 310 TYRCEASNVGKAHSDYMLY 329
Db 292 NYTCVASNKLGHNTNASIMLF 311

RESULT 11
NTRI_HUMAN
ID NTRI_HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hnt).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLN
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; AF126426; AAF37591.1;
DR MIM; 607938;
DR GO; GO:0008038; P:neuronal cell recognition; TAS.
```


RT "Functional domains of the poliovirus receptor.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
 RN [6]
 RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=93059689; PubMed=1331527;
 RA Zibert A., Wimmer E.;
 RT "N glycosylation of the virus binding domain is not essential for
 RL function of the human poliovirus receptor.;"
 RL J. Virol. 66:7368-7373(1992).
 CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
 CC cell.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
 CC delta). Secreted (isoforms beta and gamma).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=Alpha;
 CC IsoId=P15151-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=P15151-2; Sequence=VSP_002617;
 CC Name=Gamma;
 CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
 CC Name=Delta;
 CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
 CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
 CC VIRUS BINDING AND UPTAKE.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like v-type domain.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD155 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".

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 CC -----

EMBL; M24407; AAA36461.1; -;
 EMBL; M24406; AAA36462.1; -;
 EMBL; X64116; CAA45478.1; -;
 EMBL; X64117; CAA45478.1; JOINED.
 EMBL; X64118; CAA45478.1; JOINED.
 EMBL; X64119; CAA45478.1; JOINED.
 EMBL; X64120; CAA45478.1; JOINED.
 EMBL; X64121; CAA45478.1; JOINED.
 EMBL; X64122; CAA45478.1; JOINED.
 EMBL; X64123; CAA45478.1; JOINED.
 EMBL; X64116; CAA45480.1; -;
 EMBL; X64117; CAA45480.1; JOINED.
 EMBL; X64118; CAA45480.1; JOINED.
 EMBL; X64119; CAA45480.1; JOINED.
 EMBL; X64120; CAA45480.1; JOINED.
 EMBL; X64121; CAA45480.1; JOINED.
 EMBL; X64122; CAA45480.1; JOINED.
 EMBL; X64123; CAA45480.1; JOINED.
 EMBL; X64116; CAA45480.1; -;
 EMBL; X64117; CAA45480.1; JOINED.
 EMBL; X64118; CAA45480.1; JOINED.
 EMBL; X64119; CAA45480.1; JOINED.
 EMBL; X64120; CAA45480.1; JOINED.
 EMBL; X64121; CAA45480.1; JOINED.
 EMBL; X64122; CAA45480.1; JOINED.
 EMBL; X64123; CAA45480.1; JOINED.
 EMBL; AC068948; AAF69803.1; -;
 PIR; A43024; RWHUED.
 PIR; S12048; RWHUED.
 Genew; HGNC:9705; PVR.
 MIM; 173850; -;
 GO; GO:0005737; C:cytoplasm; TAS.
 GO; GO:0005615; C:extracellular space; TAS.
 GO; GO:0016021; C:integral to membrane; TAS.
 GO; GO:0004872; F:receptor activity; TAS.
 GO; GO:0007125; P:invasive growth; TAS.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 3.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Antigen; Alternative splicing; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 218 218
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPLIC 340 384
 FT VARSPLIC 331 331
 FT VARSPLIC 332 384
 FT VARSPLIC 385 392
 FT VARSPLIC 393 417
 FT VARIANT 67 67
 FT VARIANT 340 340
 FT SEQUENCE 417 AA; 45302 MW; DISC012CE853169B CRC64;
 Query Match 10.5%; Score 240; DB 1; Length 417;
 Best Local Similarity 25.9%; Pred. No. 5; Se-10;
 Matches 107; Conservative 53; Mismatches 177; Indels 76; Gaps 17;

QY 14 AAAAAAPGCLRLRLILLIFSAALPTGQGMLFKDVTV-----IEGEVATISQ 65
 DB 2 ARAMAAWPLLVLALLVLSNP-----PPGTG-----DVVQAPTQVPGFLGDSVTLPCY 50
 QY 66 V---NKSDSDSVIQLL---NPNRQTIYPRDFPLKDSRFQLNFSSELKVSITNYS--- 115
 DB 51 LQVPMNVTHVQLTWARGESGSMVHFQTQGPSYSESKRLEFVAARLGAELRNASLRM 110
 QY 116 ----ISDEGRYFCQLYTDPQESYTT---ITVLVPRNLMIDIQKDTAVEGEIEV-NCT 167
 DB 111 FGLRVEDEGNYTC-LFVTPPQGSRSVDIWLRLAKPQN-TAEVQK-VQLTGFVPNARCV 167
 QY 168 AMASKPATIRWFKGNTELKXSEVEEW-SDMYTVTSQMLKVKHEDDGVVPCQVEHPA 226
 DB 168 STGGPPAQLTWHSIDLGMPNTSQVPGFLSGTVTVTSLWILVPSQVDGKNVTCCKVEHS 227
 QY 227 VTGNLQTRYLEVQYKPVQHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVWRVDE 286
 DB 228 FEKPOLLTWNLTVYYPPEVSIIS-GVDNNWYLCQNEA-TLTCARSNPEPTGYNWSTMG 285
 QY 287 MPQHAVLSGNLFINNKNKTDNGTYRCEASNTVGAHSDYMLYVDPPPTTIPPTTTTT 346
 DB 286 LPPFAVAQAQLLRPVDPKPIPTLTCNVNVALGARQAEALTQVKEGPPS----- 335
 QY 347 TTTTITLTITDSRAGEEGSIRAVDHAVIGGVAVVVFAMLCLLIILGRYF 399
 DB 336 -----EHSGISR--NAIIFVLGLVLF---LILLIGIYF 365

DR PIR: B44194; B44194.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 3.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 85 85
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT CARBOHYD 386 392
 FT VARSPLIC 393 417
 FT VARSPLIC 417 417
 FT SEQUENCE 417 AA; 45464 MW; 45464 MW; DA4AD0F64D2F6E1F CRC64;
 Query Match 10.7%; Score 244; DB 1; Length 417;
 Best Local Similarity 23.5%; Pred. No. 2.8e-10;
 Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;
 QY 13 AAAAAAAPPGLRLRLLLLFSAALPTGCGQLFTKQVTV--IGEVATISC--QVVK 68
 Db 2 ARTMAAAPP-----LLTLLELSWPPPTGDIIVQAQTPQVGLGSDVTPCYLQVPG 55
 QY 69 SDDSVQLLNPNR-----QTIYFRDPRPLKDSRFQLLNSSSLKSLVNLTVS-----I 116
 Db 56 MEETHVSQLTWSRHGSGSMVAFHOTQNGYSEPKLEFVAARLGTGLDASLUMGLRV 115
 QY 117 SDEGRFECOLYDPPQESYTT---ITVLVPRNIMIDIQDTAVEGEEIEV-NCTAMASK 172
 Db 116 EDEGNYTC-LFVTFPGQSRSDIWLRLAKPN-TAEVQK-VQLTGKPPVAVRCVSTGCR 172
 QY 173 PATTIRWFKGNTLKGSEVEE-----WSDMYTVTSQMLKVHKEDDGVPIQVVEHPAVT 228
 Db 173 PPAHITW---HSLDGMNPTSQAQPLSTVTVTLNLVPSQVDSQVCKVEHESPE 229
 QY 229 GNLQFQVLEQYKPVQVHIOMTYPLQGLTREGDALELTCEALGKQPVMVTVVRVDDEMP 288
 Db 230 KPQLLTALVLTYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNEPTGYNNWSTWTGGLP 287
 QY 289 QHVLVSGNLFNNLNKTDNGYRCASNIVGKAHSDYMLYYPPTPIPTPTTTTTTTTT 348
 Db 288 PFVAQGAQLLRPVDKPTNTTFICNVNVALGARQALTVQKGGPPSPSGMSN----- 343
 QY 349 TTTTITLTITDSRAGEEGSIRAVDHVIGGVVAVVVFAMLLLIIL-----GRYFAHK 403
 Db 344 -----IIIFLLIGVILLTLGIGGVYFYR 369
 QY 404 GT-----YFTHAKGADDAADATAIINAEAGGNNSEKKE 439
 Db 370 CSREPLWCHLSPSSEERASA-----SANGYISYSDVSR 404
 RESULT 5
 FVR2_HUMAN
 ID FVR2_HUMAN STANDARD; PRT; 538 AA.
 AC Q92692; O75455; Q96J29;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
 DE mediator B) (HvEB) (Nectin 2) (CD112 antigen).
 GN PVRL2 OR PRR2 OR HVEB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95347610; PubMed=7622062;
 RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
 RA "The human PRR2 gene, related to the human poliovirus receptor gene
 RA (PVR), is the true homolog of the murine MPH gene.";
 RL Gene 159:267-272(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=98321161; PubMed=9657005;
 RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
 RA "A cell surface protein with herpesvirus entry activity (HvEB) confers
 RA susceptibility to infection by mutants of herpes simplex virus type
 RA 1, herpes simplex virus type 2, and pseudorabies virus.";
 RL Virology 246:179-189(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman A.C., Young A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 31-538 FROM N.A.
 RA Yoshiura K., Murray J.C.;
 RA "A transcriptional map in the region of 19ql3 derived using direct
 RA sequencing and exon trapping";
 RL Submitted (JAN-1998) to the ENBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 449-538 FROM N.A.
 RX MEDLINE=99449047; PubMed=10520737;
 RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 RA Ashworth L.K., Van Bockmeier F.M., Dawkins R.L.;
 RA "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
 RA PEREC1";
 RL DNA Seq. 9:89-101(1998).
 CC -!- FUNCTION: RECEPTOR FOR ALPHAPERSESVIRUS (HSV-1, HSV-2 AND
 CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC IsoId=Q92692-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;

QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-GYDDNNYLGRSEAI-ITCDVRSNPE	281
QY	275	PVMYTVRWV	DDMQHVLSPGNFNNLNKTDNGTVRCEASNIVGKAHSDYMLVYVDP	334
DB	282	PTDYDWS	TSGTGFASAVAQSQLLVHSVDWMVNTTFTCTATNAVGTGRAEQVILVRESP	341
QY	335	TTIPPTTTTT	TTTTTTTTTTTTLTITSDRAGESSIRAVDHAVIGGVAVVV	385
DB	342	ST-----	AGAGATGGI-----IGGIIAII	361
RESULT 4				
QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-GYDDNNYLGRSEAI-ITCDVRSNPE	281
QY	275	PVMYTVRWV	DDMQHVLSPGNFNNLNKTDNGTVRCEASNIVGKAHSDYMLVYVDP	334
DB	282	PTDYDWS	TSGTGFASAVAQSQLLVHSVDWMVNTTFTCTATNAVGTGRAEQVILVRESP	341
QY	335	TTIPPTTTTT	TTTTTTTTTTTTLTITSDRAGESSIRAVDHAVIGGVAVVV	385
DB	342	ST-----	AGAGATGGI-----IGGIIAII	361
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).				
QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-GYDDNNYLGRSEAI-ITCDVRSNPE	281
QY	275	PVMYTVRWV	DDMQHVLSPGNFNNLNKTDNGTVRCEASNIVGKAHSDYMLVYVDP	334
DB	282	PTDYDWS	TSGTGFASAVAQSQLLVHSVDWMVNTTFTCTATNAVGTGRAEQVILVRESP	341
QY	335	TTIPPTTTTT	TTTTTTTTTTTTLTITSDRAGESSIRAVDHAVIGGVAVVV	385
DB	342	ST-----	AGAGATGGI-----IGGIIAII	361
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).				
QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-GYDDNNYLGRSEAI-ITCDVRSNPE	281
QY	275	PVMYTVRWV	DDMQHVLSPGNFNNLNKTDNGTVRCEASNIVGKAHSDYMLVYVDP	334
DB	282	PTDYDWS	TSGTGFASAVAQSQLLVHSVDWMVNTTFTCTATNAVGTGRAEQVILVRESP	341
QY	335	TTIPPTTTTT	TTTTTTTTTTTTLTITSDRAGESSIRAVDHAVIGGVAVVV	385
DB	342	ST-----	AGAGATGGI-----IGGIIAII	361
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).				
QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-GYDDNNYLGRSEAI-ITCDVRSNPE	281
QY	275	PVMYTVRWV	DDMQHVLSPGNFNNLNKTDNGTVRCEASNIVGKAHSDYMLVYVDP	334
DB	282	PTDYDWS	TSGTGFASAVAQSQLLVHSVDWMVNTTFTCTATNAVGTGRAEQVILVRESP	341
QY	335	TTIPPTTTTT	TTTTTTTTTTTTLTITSDRAGESSIRAVDHAVIGGVAVVV	385
DB	342	ST-----	AGAGATGGI-----IGGIIAII	361
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).				
QY	106	ELKVSILNNVSI	SDGRYFCQLYTDP--PQESYTTITVLVPPNLMIMDIQKDTAVEGEETE	163
DB	113	DATLAFGLRLR	VEDEGNYTCEPATFNGTRRGVTWLRVIAQPEN-----HAEAEQVET	163
QY	164	V-----	NC TAMASKPATIRWFKG-NTELKGKSEVEEWSMDYTVTSQMLKVHKEDD	214
DB	154	IGPOSVAVARC	VSTGGRPPARITWISSJGGEAKDTQEPGIQAGTVTIISRYSLVFPVGRAD	223
QY	215	GVPVICQVHEP	AVTGNLQTSYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ	274
DB	224	GVKYTCRVEH	SEEPILLPVTSVSRVPEVIS-G	

297 NLFINN-LNKNDGNTYCRASNIVGKARSDYMLVYDPTTPPTTPPTTTTTTTTTTTTTTIL 355
 299 TLFFKGRINSLAGTYICETNPIGTRSGQGVENVITFPFYPSPPE----- 344
 356 TIIITDSRAGEGSTRADVHGVIGVGVAVVFMCLIIILGRYFA----RH--KGYTF- 408
 345 ---HGRRAG-----PVPTAIGGVAGSI---LLVLIWVGIVVVALRRRRTFKGDYSTK 392
 409 -----HEAKGA-----DDAADADTAIINAGGQNNSEKKE 439
 393 KHYVNGYSKAGIPQHPHPAQNLOYPDSDDEKKA---GPLUGSSYEEEEEE 442
 DB NCBI_TaxId=10090;
 [1]
 SEQUENCE FROM N.A. (ISOFORM ALPHA).
 MEDLINE=92219365; PubMed=1560525;
 Morrison M.E., Racaniello V.R.;
 "Molecular cloning and expression of a murine homolog of the human
 poliovirus receptor gene.";
 J. Virol. 66:2807-2813(1992).
 [2]
 SEQUENCE FROM N.A. (ISOFORM BETA).
 STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=94179228; PubMed=8132563;
 Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
 "Amino acid residues on human poliovirus receptor involved in
 interaction with poliovirus.";
 J. Biol. Chem. 269:8431-8438(1994).
 [3]
 SEQUENCE FROM N.A. (ISOFORM BETA).
 STRAIN=EVB/N; TISSUE=Colon;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
 Bosak S.A., McGowan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 CHARACTERIZATION.
 MEDLINE=99214397; PubMed=10196354;
 Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
 "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
 mediates entry of pseudorabies virus but not herpes simplex virus
 types 1 and 2.";

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 9.38761 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187b-2
Perfect score: 2283
Sequence: 1 MASVLPSSGSCAAAAA.....AIINAEQQNNSBEKKEYFI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	266.5	11.7	515	1 PVRI_PIG	Q9176 sus scrofa
2	256.5	11.2	517	1 PVRI_HUMAN	O15223 sus scrofa
3	247.5	10.8	530	1 PVR2_MOUSE	P32507 mus musculus
4	244	10.7	417	1 PVR_CERAE	P32506 cercopithec
5	242.5	10.6	538	1 PVR2_HUMAN	Q92692 homo sapien
6	240	10.5	417	1 PVR_HUMAN	P15151 homo sapien
7	239	10.5	515	1 PVRI_MOUSE	Q91kf6 mus musculus
8	239	10.5	1088	1 NCAL_XENLA	P16170 xenopus lae
9	231	10.1	344	1 NTRI_MOUSE	Q99p10 mus musculus
10	230	10.1	344	1 NTRI_RAT	Q62178 rattus norv
11	228	10.0	344	1 NTRI_HUMAN	Q9p121 homo sapien
12	223.5	9.8	837	1 NCW2_MOUSE	Q35136 mus musculus
13	223	9.8	1092	1 NCW2_XENLA	P16335 xenopus lae
14	222	9.7	837	1 NCW2_HUMAN	O15394 homo sapien
15	222	9.7	1242	1 NPIN_MOUSE	Q9qz57 mus musculus
16	219	9.6	337	1 OPMC_CHICK	Q98892 gallus gall
17	218.5	9.6	345	1 OPMC_BOVIN	P11834 bos taurus
18	217.5	9.5	583	1 C166_MOUSE	Q61490 mus musculus
19	217	9.5	588	1 C166_CHICK	P42292 gallus gall
20	216.5	9.5	345	1 OPMC_HUMAN	Q14982 homo sapien
21	213.5	9.4	4391	1 PGBM_HUMAN	P98160 homo sapien
22	210.5	9.2	345	1 OPMC_RAT	P32736 rattus norv
23	209	9.2	338	1 LAMP_CHICK	Q98919 gallus gall
24	209	9.2	353	1 CEPU_CHICK	P97798 mus musculus
25	208	9.1	1493	1 NEOL_MOUSE	P20773 homo sapien
26	207	9.1	847	1 CD22_HUMAN	Q9uhc6 homo sapien
27	206.5	9.0	1331	1 CTA2_HUMAN	P06731 homo sapien
28	206	9.0	702	1 CEAS_HUMAN	Q13449 homo sapien
29	205.5	9.0	338	1 LAMP_HUMAN	P97710 r protein-t
30	205.5	9.0	509	1 SHS1_HUMAN	P43121 homo sapien
31	205.5	9.0	646	1 MU18_HUMAN	Q92859 homo sapien
32	205.5	9.0	1461	1 NEOL_HUMAN	Q05793 mus musculus
33	204	8.9	3707	1 PGBM_MOUSE	

34	203.5	8.9	862	1	CD22_MOUSE
35	202	8.8	1377	1	NEOL_RAT
36	202	8.8	1443	1	NEOL_CHICK
37	199.5	8.7	338	1	LAMP_RAT
38	199.5	8.7	1241	1	NPIN_HUMAN
39	197.5	8.7	1234	1	NPIN_RAT
40	197	8.6	583	1	C166_HUMAN
41	196	8.6	1091	1	NCAL_CHICK
42	194	8.5	506	1	SHS1_BOVIN
43	193	8.5	761	1	NCAL_HUMAN
44	193	8.5	764	1	ICCR_DROME
45	193	8.5	848	1	NCAL_HUMAN

P35329	mus musculus
P97603	rattus norv
Q90610	gallus gall
Q62813	rattus norv
O60500	homo sapien
Q9r044	rattus norv
Q13740	homo sapien
P13590	gallus gall
O46631	bos taurus
P13592	homo sapien
Q08180	drosophila
P13591	homo sapien

ALIGNMENTS

RESULT 1
PVRI_PIG
ID PVRI_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRL1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Kruppenacher C., Eisenberg R.J., Cohen G.H.;
RT "Porcine HvEC, a member of the highly conserved HvEC/nectin 1 family, is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001)
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPEVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF308632; AAG30281.1; --
DR HSSP; P06907; 1NEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; 1g_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141
FT IG-LIKE V-TYPE.
FT DOMAIN 145 243
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334
FT POLY-GLU. 437 443

Db 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR-----GPVVVTVWEGNPNVITCEVFAH 425

Qy 273 PQPVWVTVWRVDDMPQH-----AVLSGP---NIFINNLTNDGTGRCEASNIIVGKAHS 324

Db 426 PR-AAVTFWRDGLPSSNFGNFIKYSPTSSLEVNPDSNDFGNCTAINIGHEFS 484

Qy 325 DYMLVYVDPPTTIPPTTT 364

Db 485 EFILVQADTPSS---PAIRKVEPYSSTVMIVDFDPDSTGG 521

RESULT 14

T42633

connectin/titin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42633

R:Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma Biochem. Biophys. Res. Commun. 223, 160-164, 1996

A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re

A:Reference number: 222221; MUID:96254045; PMID:8660363

A:Accession: T42633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4162 <YAJ>

A:Cross-references: EMBL:D83390; NID:g1513029; PIDN:BAAL1908.1; PID:g1513030

A:Experimental source: breast muscle

C:Keywords: skeletal muscle

Query Match 10.1%; Score 230.5; DB 2; Length 4162;

Best Local Similarity 23.9%; Pred. No. 1.3e-07;

Matches 86; Conservative 60; Mismatches 155; Indels 59; Gaps 15;

Qy 12 CAAAAAAPPGLRLRLLLLSAALIPFGDQNLFTKDVTVIEGEVATISQVKNKSD 71

Db 3453 CIGSVTLRAPPTFVKL-----SDTVVVGTEIQLQAAGEAQP 3491

Qy 72 SVIQLLNPNROTIFRDFRLKDSRFQLNFSSELKVSILTNVISIDEGRYFCOLYTD 131

Db 3492 ISVLWLKDKGEII-----RESENLVSYSENVASLKGNAEPTNAGKYICQIKNDAG 3543

Qy 132 -QSYTTITVLVPPRNLMIDIQDQAVE---GEEIEVNCMTAMASKPATIRWFKGNTELK 187

Db 3544 FOECFAKLTVLEP---AVIVKPGPVKVTAGDSCTLECT-VDGTPELTARWFKGNELS 3598

Qy 188 GKSEVEEWSDMYTVTSQMLKVKHEDDG---VPVICOVHEPAVTGNLQ-TORYLEYQYKP 243

Db 3599 TDHXY-KISFFNNKVSGLKILNAGLEDSGYTFEVKNSVGKSCSTASLQVSDRIMPSPFR 3657

Qy 244 QVHIQWPTYLQGLTRGDALELTCEAIGKQPQVMVTVVRVDDMPQ---HAVLSGP--N 297

Db 3658 K-LKETY-----GQLGSSAVLECKYVGP-FILVSWFHGDQGITSGDKYQATLTDNCS 3709

Qy 298 LFINNLKNDGTGRCEASNIIVGKAHSYMLVYDPPPTTI---PPPTTTTTTTTTTTTT 355

Db 3710 LKVNGLQESDMGTYSCTATNAGSDCSAFLSVREPPSPVKXPEPNVLSGENITFTSIV 3769

RESULT 15

I56551

neurotramin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: I56551

R:Struyk, A.F.; Canoll, P.D.; Wolfsgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L. J. Neurosci. 15, 2141-2156, 1995

A:Title: Cloning of neurotramin defines a new subfamily of differentially expressed neur

A:Reference number: I56551; MUID:95198094; PMID:7891157

A:Accession: I56551

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-344 <RES>

A:Cross-references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termil

Query Match 10.1%; Score 230; DB 2; Length 344;

Best Local Similarity 26.2%; Pred. No. 5.6e-09;

Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;

Qy 29 LLLLFSAALIPFGDQNLFTK---DVTVIEGEVATISQVKNKSDSDSVIQLLNPNROT- 84

Db 19 LRLFLVPTGVPVRSGDATFPKAMDNVTVROGESATLRCTI---DNRVTVAVLNLNRSTIL 75

Qy 85 YFRDFRLKDSRFQLNFSSELKVSILTNVISIDEGRYFCOLYTD-PPOSSYTTITVLVP 143

Db 76 YAGNDKWCLEDPVLLSNTQTQYSIEIQNVVDVDEGYTCVQTDNHPKTSRVHLIVQVS 135

Qy 144 PRNLMDIQDQAV-EGEEIEVNCMTAMASKPATIRWFKGNTELKSKSEVEEWSDMYTVT 202

Db 136 PK-IVEISSDISINEGNNISLACIA-TGRPEPTVTVRHHISPKAVGVSEDEYLEIQGIT 192

Qy 203 SOLMLKVH---KEDDGVPIVCQVEHPAVTGNLQRTORYLEYQYKPVHIQWPTYLQGL-TR 258

Db 193 REQSGEYECASNDVAAPVVRVN-----VTNYPPIYS-----EAKGTGP 234

Qy 259 EGDALLETCEAIGKQPQVMVTVVRVDDMPQ-----HAVLSGENLFINNLKNDNG 309

Db 235 VGQKGTQLQCEASAVPS-AEFQWFKDDKLVGEGKKGVKNRPFSLRTTF--NVSEHDYG 291

Qy 310 TYRCEASNIIVGKAHSYMLY 329

Db 292 NYTCVASNKLIGHTNASIMLF 311

Search completed: May 27, 2004, 09:32:23

Job time: 14.7776 secs

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227 VTGNIQTORYLEVQYKPOVHITQMTYPIQGLTREGDALELTCEAIGKPPQPVMTVWRVDD 386
Db 228 FBKQQLLTWNLTVYYPPEVSIS-GYDNWNWLGQNEA-TLCTDARSNEPPTGYNWSITMGP 285
QY 287 MQQHAVLGGPNLFINNLKTDNGTYRCEASNIYKGAHSDYMLXYDPTTPIPPPTTTTT 346
Db 286 LPFFAVAQGAQLLRPVDKPINTTLICNVNLTALGARQAEULTVQVKEGPP----- 334
QY 347 TTTTITLTITIDSRAGECSIPAVDHVIGGVAVVVFAMCLLIILGRYP 399
Db 335 -----SEHSGMSR--NALIFVLGLTFV---LILLGIGIVF 365

```

RESULT 13
IUMNLN
neural cell adhesion molecule long domain form precursor - African clawed frog
N:Alternate names: NCAM-180
N:Contains: neutral cell adhesion molecule, short domain form (NCAM-140)
C:Species: *Xenopus laevis* [African clawed frog]
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C:Accession: S09600
R:Krieger, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A:Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A:Reference number: S09600; MUID:90098871; PMID:2481269
A:Accession: S09600
A:Molecule type: mRNA
A:Residues: 1-1088 <KRI>
A:Cross-references: EMBL:M25696; NID:g214609; PID:AAA49909.1; PID:g214610
A:Note: the authors translated the codon AAA for residue 970 as Leu
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Comment: Several forms of NCAM are produced by alternative splicing.

C:Genetics:
A:Gene: NCAM
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin domain
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal peptide
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LF>
F:20-803/1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <LF>
F:20-705/Domain: extracellular #status predicted <EXT>
F:34-95/Domain: immunoglobulin homology <IM1>
F:129-188/Domain: immunoglobulin homology <IMW2>
F:149-153/Region: heparin binding #status predicted
F:158-162/Region: heparin binding #status predicted
F:225-284/Domain: immunoglobulin homology <IMW3>
F:317-381/Domain: immunoglobulin homology <IMW4>
F:413-475/Domain: immunoglobulin homology <IMW5>
F:512-589/Domain: fibronectin type III repeat homology <FN3A>
F:618-679/Domain: fibronectin type III repeat homology <FN3B>
F:706-723/Domain: transmembrane #status predicted <TM>
F:724-1088/Domain: intracellular #status predicted <INT>
F:41-93,136-186,223-282,323-379,420-473/Disulfide bonds: #status predicted
F:1219,1310,141,217,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 239; DB 1; Length 1088;
Best Local Similarity 26.2%; Pred. No. 5.6e-09;
Matches 89; Conservative 62; Mismatches 147; Indels 42; Gaps 15;

```

50 KDVTVIEGEVATISC--OVNKS--DDSVIQLLN-----PNRQTIVPRDFRPLKDSRQL 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 KDTQIVNVPTTQARQLRWNTANMAESVLSCDADGFFDPEISMLWKGEPIEDGE-EK 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100 LNFSSSELKVLSTNVGISDEGRFYCOLYDTPQESVYTTITVLVPPRNLMIQDKDTAVEG 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
258 ISFNEDQSEMTIHVHKDDEAEVSC-IANNQAGEBAETILLKYAKPKITTVENKTAVEL 316
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
160 EEEVNTAMASKPATIRW-----FRGNTLKGKSEVEBSWDMYTTVSQMLKVKHE 212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
317 DEITLTCEA-SGDPIPSITWRTAVRNISSEATTLDGHIWVKEHIRM---SALTUKDIQY 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
213 DDGVPVICQVEHPAVTGNLTORYLEVQYKPOVHIQMTYPIQGLTREGDALELTCEAIGK 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      108 AKQSTGQDTEAELODATALHGLTVEDEGNVTCBFAFPKGVGRGWTWLRVIAKPN-QA 166
QY      150 DIQKDTAVEGEIEVNCATAMASKPATTIRWFKG-NTELKKGKSEVEEWSDMYTVTSQMLK 208
Db      167 EAQKVTFSQDPTTVALCTSKGKPPARISWLSLSDWEAKETQVSGTLAGTIVTSRFTLV 226
QY      209 VHKEDDGVVICQVEHPATVGNLQRYLEYQKQVHQMITYPQGLTREGDALELTC 268
Db      227 PSGRADGVTVTCVKBHSEFEFALLPVTLSVRYPPEVSIS-GYDDNWVLGRDTA-TLSCD 284
QY      269 AIGKQPVMVTVVRVDDMPQHAVLSGPNLFNNLNKTDNGTYRCEASNVKASHDYM 328
Db      285 VRSNEPTGYDWSITSGFPTSAVAGGSQVLIHVDLSFNFTFVTVTVNAVGNRAEQVI 344
QY      329 YVDPPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 388
Db      345 FVRETPNT-----AGAGATGGI-----IGGIIAIIATA 373
QY      389 LCLLLIILGRYPARHKGTYFTHEAKGADDAADAD-----TALINAE-----G 429
Db      374 VAATGILICRQKQKQ-----LOGAEDEDELEGPPSYKPTPKAKLEAQEMPSQLFTIG 428
QY      430 GQNNSEKKEYF 441
Db      429 ASEHSPKTPYF 440

RESULT 10
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: B44194
R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A:Title: A second gene for the African green monkey poliovirus receptor that has no puta
A:Reference number: A44194; MUID:93059651; PMID:1331508
A:Accession: B44194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: GB:S48817
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IM>

Query Match      10.6%; Score 241.5; DB 2; Length 392;
Best Local Similarity 24.0%; Pred. No. 1e-09;
Matches 101; Conservative 60; Mismatches 176; Indels 81; Gaps 16;

QY      13 AAAAAAAPPGLRLRLRLLLLSAALIPFGQNLFTKDVTV--LEGVATISC--QUNK 68
Db      2 ARTWAARWPP-----LLLTLELSWPPGGTGIIVQAPTQVPGFLGDSVTLPCYLVQ 55
QY      69 SDDSVIQLINPNR-----QTIYFRDFRPLKDSRFOLLNFSSELKVSILTNSV-----I 116
Db      56 MEETHVSLQTSWRHSGESSMAVFHTQCPNVPSEKRLFEVFAARLGTDLRDLASLRFGLRV 115
QY      117 SDEGRYFCQLYTDPQESYTT---ITVLVPPRNLMIDIKQDTAVEGEIEV-NCTAMASK 172
Db      116 EDEGNVTC-LFVTFPQGSRSVDIWLRLAKQN-TAEVQK-VOLTGPVPVAVRCSVGTGR 172
QY      173 PATTIRWFKGNTELKKGSEVEE-----NSDMYTVTSQMLKVKHEDDGVPLVCQVEHPAVT 228
Db      173 PPAHITW---HSDLGMPNTSQAGFISGTVTVLSLWILVPSQVQDGKSVTCVKEHESFE 229
QY      229 GNLTQRYLEYQYKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDDMP 288
Db      230 KPQLLTVNLTYYYPPEVSIS-GYDNNWVLSQNEA-TITCDARSNPETGYNWSVTMGPLP 287
QY      289 QHAVLSGPNLFINNLKTDNGTYRCEASNVGKAHSDYMLYVYVDPPTTIPPTTTTTTTT 348
Db      288 PFAVAQAQLLIRPVDKPINTTTFICVTNALGARQAELTVQVKGPSPFSGMSSN----- 343
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QY      349 TTTTILITITDSRAGERGSIRAVDHAIVGIGVAVVVFAMLCGLLIL-----GRYFARHK 403
Db      344 -----IIIFILGIVILLTLLGIGVYFYRSR 369

RESULT 11
RWHPUD
poliovirus receptor splice form delta precursor - human
N:Alternate names: poliovirus receptor H20B
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A43024; B31496
R:Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Izuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A:Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A:Reference number: S12048; MUID:91006015; PMID:2170108
A:Accession: A43024
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: EMBL:X64116
A:Note: 67-A'a was also found
R:Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A:Reference number: A90910; MUID:89168426; PMID:2538245
A:Accession: B31496
A:Molecule type: mRNA
A:Residues: 1-66, 'A' 68-392 <MEN>
A:Cross-references: GB:M24406
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:1-20/Domain: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F:21-392/Product: signal sequence #status predicted <SIG>
F:21-343/Domain: poliovirus receptor delta #status predicted <MAT>
F:42-125/Domain: extracellular #status predicted <EXT>
F:159-223/Domain: immunoglobulin homology <IMM1>
F:259-314/Domain: immunoglobulin homology <IMM2>
F:344-367/Domain: immunoglobulin homology <IMM3>
F:368-392/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match      10.5%; Score 240; DB 1; Length 392;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 107; Conservative 54; Mismatches 176; Indels 76; Gaps 17;

QY      14 AAAAAAAPPGLRLRLRLLLLSAALIPFGQNLFTKDVTV-----LEGVATISC- 64
Db      2 ARMAAAWPP-----LLLTLELSWPPGGTGIIVQAPTQVPGFLGDSVTLPCY 50
QY      65 -QVKNKSDSVIQLINPNR-----QTIYFRDFRPLKDSRFOLLNFSSELKVSILTNSV----- 115
Db      51 LQVPNMEVTHVSQLTWTRHGESGSMVFTQGPVSYSERKLEFVAARLGAELRNASLRM 110
QY      116 -----ISDEGRYFCQLYTDPQESYTT---ITVLVPPRNLMIDIKQDTAVEGEIEV-NCT 167
Db      111 FGLRVEDEGNVTC-LFVTFPQGSRSVDIWLRLAKQN-TAEVQK-VOLTGPVPVAVR 167
QY      168 AMASKPATTIRWFKGNTELKKGSEVEE-SDMYTVTSQMLKVKHEDDGVPLVCQVEHPA 226
Db      168 STGGRPPAQLTHSDLGMPNTSQAGFISGTVTVLSLWILVPSQVQDGKSVTCVKEHES 227
QY      227 VTGNLTQRYLEYQYKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVVRVDD 286
Db      228 FEKPOLLTVNLTYYYPPEVSIS-GYDNNWVLSQNEA-TITCDARSNPETGYNWSVTMG 285
QY      287 MPQHAVLSGPNLFINNLKTDNGTYRCEASNVGKAHSDYMLYVYVDPPTTIPPTTTTTT 346
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164  IGPQSVAVARCVSTGCRPPARIITWISLGLGEAKDTQEGIGAQGTVTITISRYSLVPVGRAD 223
215  GVPVICOVEHPAVTGNLQTOYLEVOYKPOVHIQMTYPLQGLTFREGDALELTCEAIKPKQ 274
224  GVKVTCRVEHSEFEPIILLPTLSRVYPPVSVIS-GYDDNWYLGSRSAI-LTCDVRNSNP 281
275  PVMVTWVRVDEMPQHAVLSGPNLFNNLNKNTDNGTYRCEASNIIVGKAHSDYMLYVYDPP 334
232  PTDYDSTTSVGVFPASAVAQGSQLLVHSVDRMVTTFICTATNAVGTGTRAEQVILVRESP 341
335  TTTPPTPTTTTTTTTTTTTTTTTTTTTTITDSRAGEBGSIRAVDHAHVIGGVAVVV 385
342  ST-----AGAGATGGI-----IGGIIAAII 361

RESULT 6
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C/Species: Carcophithacus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: A44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no put:
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: A44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-417 <KOI>
A/Cross-references: GB:S48777
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: transmembrane protein
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 244; DB 2; Length 417;
Best Local Similarity 23.5%; Pred. No. 7.2e-10;
Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

QY 13 AAAAAAAPPGLRLRLILLFSAALIPICGQNLTKQVTV--IEGEVATISC--QYNK 68
DB 2 ARTMAAAWPP-----LLLTLLLELWPPPTGDIIVQAPTQVPGFLGDSVTLPCYLQVPG 55
QY 69 SDDSVIQLLNPNR-----QTIYFRDPRFLKDSRFQLNFSSSELKVSLTNVS-----I 116
DB 56 MBETHVSQLTWSRHGSGSMANVFHQYQGNYSPEKLEFVAARLGTFLRDASIRMFCLRV 115
QY 117 SDEGRFYCOLYTDPPQESYTT---ITVLVPPRLMIDIOKDTAVEGEIEIV-NCTAMASK 172
DB 116 EDEGNNTYC-LFVTFPGQSRSDVILWEVLAKPON-TAEVQK-VQLTGKPVVARCVSTGGR 172
QY 173 PATTIRWFKNGETLKGKSEVE-----WSDMYTVTSQMLMKVHKEDDGVPVICQVEHPAVT 228
DB 173 PPAHITW---HSDLGMPNTSQAPGLSTGTVTISLWILVPSQVDGKSVTCKEVESFE 229
QY 229 GNLQTOYLEVOYKPOVHIQMTYPLQGLTFREGDALELTCEAIKPKOPVMTWVRVDEMP 288
DB 230 KPQLLTWNLTVYYPPEVSVIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTNGPLP 287
QY 289 QHIAVLSGPNLFNNLNKNTDNGTYRCEASNIIVGKAHSDYMLYVYDPPPTTPPTTTTTTTT 348
DB 288 PFVAQAQGLLRPVDKPIINTTFICNVTNALGARQAEITVQVKEGPPSEPSGMSN---- 343
QY 349 TTTTITLITDSRAGEBGSIRAVDHAHVIGGVAVVVFAMLCILIL-----GRYPARIK 403
DB 344 -----IIFLILGIVILLTLGLIGVYFYSR 369
QY 404 GT----YFTHKAGDADAADATTAIARGGONNSEKXE 439
DB 370 CSREFLWCHLSPSSEEHASA-----SANGYISYSDVSRE 404

RESULT 7
HLMSP3

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R.Sultson, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <WtL>
A:Cross-references: EMBL:Z47068; PIDN:CAA97335.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone F15G9
R;Kershaw, J.

submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <Wt2>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T09B9
C;Genetics:
A:Gene: CESP:F15G9.4a
A:Map position: X

A;Intronous: 857/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
S; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
I; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;

Query Match 11.5%; Score 263.5; DB 2; Length 5175;
Best Local Similarity 24.6%, Pred. No. 7.6e-10;
Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;

Qy 52 VTVIEGEVATISCVWNKSDDSVIOLLNPNTQTIVYFRDFRL-----KDSTRFOLLNFSSSEL 107
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2200 VTAIKGGALPKPCID--DDK----NFKGLIWLRYNQPIDLEAEARITRL---SNDR 2249

Qy 108 KVSILTNYVISDEGRFYQLYTDPQRSYT-TITVLVPNRMLMIDIQKD-TAVSGEIEVN 165
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2250 RLTILNVTEHDGYSCKRVNDAGENSFDFAKITVLVPTTIIMLDKKNKTTAVEHSTVTLS 2309

Qy 166 CTAMASKPATITIRFWKG-----NTELKGKSEVEWSDMYTVTSOLMKLVHK 211
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2310 CPA-TGRPEPDIWFVKDGEAIHIENIAADIIPNGELN-----NOLKITRIK 2354

Qy 212 EDDGVFVICQEHPHAVTGNICTORYLEVQYPQH---IQMTYPLQGTLREGDALETCE 268
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2355 EGDAQKYTCADNSA--GSVEQQDVNNVIPIPIEKDGIPSDESQ-----QNERVVISCP 2408

Qy 269 AIGKPQPWMVVWRVDDEMPPHAFL-----SGPNLFINNKNKTDTGTGYRCEASNIYGKAHS 324
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2409 VIARP-PAKITLKAGKLQSDFEVKTSANGXQKIYLFURETDSSKYCTIANEAQTKR 2467

Qy 325 DYMLYVDPPTTIPP-----PTTTTTTTTTTTTTIIITIITDSRAE 365
Db ||| :||| :||| :||| :||| :||| :||| :||| :||| :
Dd 2468 DFKVSLVAFPDEFEPNVRRTITVNSGNPSTLHCAPKGPSPTITLWKDGAIE 2520

RESULT 3
T43290 hemicentin precursor - Caenorhabditis elegans
T43290 C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43290; T20993; T24734
R;Voegel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A>Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
A;Reference number: Z22396
A;Accession: T43290
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-5198 <VOg>
A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R,Sultson, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <MWL>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: J24734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WI2>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone T09B3
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 1371/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/3; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;
Query Match 11.5%; Score 263.5; DB 2; Length 5198;
Best Local Similarity 24.8%; Pred. No. 7.6e-10;
Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;
QY 52 VTVEIEGAVTISQVNVKNSDDSVIQLNPNRQTIYFRDRLP-----KDSRFQLNFSSEL 107
Db 2200 VTAIKGAUFPKPID-DDK-----NFKQIILWLNYPIDLEAEDARITRL-----SNDR 2249
QY 108 KVSLTNVSISDEGRYFCQLYTDPQSYT-TIFVLVPPRLMIDIQKD-TAVEGEEIVN 165
Db 2250 RLITLNVTEDEQYSCRVKNDAGENSDFKATLVLPPTIIMLDKDKNTAVEHSVTLS 2309
QY 166 CTAMASKPATITIRWFG-----NTELKGSKEVEEWSMYVTTSQMLKXVHK 211
Db 2310 CPA-TGKPEPDIWFKDGAHHENTADIPNGEL-----NQLKITRIK 2354
QY 212 EDDGVPVICQVEHPAVTGNLQTVLEVQYKQVH---IQMTYPLQGLTREGDALELTCE 268
Db 2355 EGDAGKYTCEDNSA--GSVEQDVNVNVTIPKIEKDGIPSDYESQ-----QNERVVISCP 2408
QY 269 AIGKPPQVMVTVRVVDDEMPQHAVL-----SGNLFINNLNKTDNGTYRCEASNIVGKAHS 324
Db 2409 VTARP-PAKITLWAKGQLQSDKFVKTISANGOKLYFLKURETDSKSYTCIATNEACTDKR 2467
QY 325 DYMLXYVDPFTTIPP-----PTTTTITTTTTTTTTITITIDSRAGE 365
Db 2468 DFKVSLMVAPEFDEPNVIRITVNSGNPSTLHCPAKGSPSPITWLKQNAIE 2520
RESULT 4
JC4024
poliovirus receptor-related protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C:Accession: JC4024
R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Marroc, C.; Dubi
Gene 155, 261-285, 1995
A:title: Complementary DNA characterization and chromosomal localization of a human gene
A:Reference number: JC4024; MUID:95237621; PMID:7721102
A:Accession: JC4024
A:Molecule type: mRNA
A:Residues: 1-518 cLQp>
A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAAS3980.1; PID:g732796
C:Genetics:
A:Gene: GDB:PVRR1
A:Cross-references: GDB:583951
A:Map position: 11q23-11q24
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:51-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F:356-379/Domain: transmembrane #status predicted <TMW>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.7776 Seconds
(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-2
Perfect score: 2283
Sequence: 1 MASVLPSSGSCAAAAAAA.....AIINAEGQNNSEBKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	11.7	407	T08732	hypothetical prote
2	263.5	11.5	5175	T20992	hypothetical prote
3	263.5	11.5	5198	T43290	hemocentin prote
4	248	10.9	518	JC4024	poliovirus recepto
5	247.5	10.8	530	A53437	poliovirus recepto
6	244	10.7	417	A44194	poliovirus recepto
7	244	10.7	467	HLMSF3	poliovirus recepto
8	243	10.6	725	JE00099	PRR2 delta - human
9	242.5	10.6	538	I68093	poliovirus recepto
10	241.5	10.6	392	B44194	poliovirus recepto
11	240	10.5	392	1 RHUPD	poliovirus recepto
12	240	10.5	417	1 RHUPA	poliovirus recepto
13	239	10.5	1088	1 IJLNL	neural cell adhesi
14	230.5	10.1	4162	T42633	connectin/titin -
15	230	10.1	344	I56551	neurotrophin - rat
16	226	9.9	812	B42632	cell adhesion mole
17	226	9.9	932	A42632	cell adhesion mole
18	225	9.9	7962	I38346	elastic titin - fr
19	223.5	9.8	1011	TJ3669	neuromusculin - fr
20	223	9.8	725	JE0100	neural cell adhesi
21	223	9.8	1092	1 JN0635	PRR2 alpha - human
22	222	9.7	478	I53960	PRR2 alpha - human
23	218.5	9.6	345	S03199	opioid-binding pro
24	218.5	9.6	588	A45254	surface glycoprote
25	217	9.5	588	JH0506	adhesion molecule
26	216.5	9.5	345	JC4025	opioid-binding cel
27	216	9.5	765	2 JC4025	cell adhesion mole
28	214	9.4	4391	2 A38096	perlecan precursor
29	210.5	9.2	345	2 JCI239	opioid-binding pro

30	209.5	9.2	584	2	I50419	s-gicerin precurs
31	209	9.2	338	2	JC5519	50K glycoprotein p
32	206	9.0	702	2	A36319	carcinoembryonic a
33	205.5	9.0	338	2	JC4776	limbic-system-asso
34	205.5	9.0	646	2	I38049	cell surface glyco
35	204.5	9.0	338	2	JC1238	opioid-binding pro
36	204	8.9	3707	2	I18252	heparan sulfate pr
37	203	8.9	1323	2	PN0568	connectin 3B - chi
38	202.5	8.9	862	2	I49583	differentiation an
39	202.5	8.9	868	2	A46512	CD22 homolog/B lym
40	202	8.8	847	2	JH0371	B-cell adhesion pr
41	202	8.8	1443	2	I50600	neogenin - chicken
42	199.5	8.7	1241	2	T37190	nephrin - human
43	197	8.6	583	2	I39428	alcam - human
44	196	8.6	1091	1	IUCHNL	neural cell adhesi
45	195.5	8.6	1612	2	T30805	dutt1 protein - mo

ALIGNMENTS

RESULT 1

T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08732
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:CROSS-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZp566B0846
C:Genetics:
A:Note: DKFZp566B0846.1

Query Match 11.7%; Score 268; DB 2; Length 407;
Best Local Similarity 26.7%; Pred. No. 1.4e-11;
Matches 84; Conservative 60; Mismatches 123; Indels 48; Gaps 13;

QY	120	GRYFCOLYTD-POESYTTITVLVPRNLMIDIOKTAVEG--EEIVNCTAMASKPAT	175
DB	2	GKXICKAVTFPLGNAGSSTTVLVEPTVSLIK-GPDSLIDGNETVAAICIAATGKPA	60
QY	176	TTRWPKGNTELKSGSEVEWSDMY-----TVTSQLMLKVHKEDDGVFVICOVEHPAVTGN	230
DB	61	HIDW-EGDL-----GEMESTTTSFPNETATILISQYKLPFTRFARGRRITCVVKGHPALEKD	114
QY	231	LQTRVLEVOYKQVHIQWYTPLOGLTRGDALELTCEAIGKPPQPMVTVRVDDMPQH	290
DB	115	KYSFIDLIQYAPEVSVTVGDGNWFWVGRKG--VNLKCNADANPPFPKSVWSRLDGQWPDG	172
QY	291	AVLSGPNL-FINNLKNTDNGTYRCEASINIVGKASDYMIVYVDDP-PTT	342
DB	173	LLASDNLHFVHPLFNYSGVVICKVTSLGORSQKVIYISDPTTTTTLQTIQWHPST	232
QY	343	TTTTTTTT-----TTTILTITDSRAGSGSIRAVDHAIVGIVGVVAVFAMCLLI-	393
DB	233	ADIEDLATEPKLPPLSLATI-----KDDTIATIASVVGALFVLVSLAGLIFC	285
QY	394	-----ILGRYFAH	402
DB	286	YRRRTFRGDYFAKN	300

RESULT 2

T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733

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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-84

Query Match      90.9%; Score 2059; DB 10; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLILLLLFACCCWAPGAGNLSQGYWQEQDLELGLTAPLDEAISSTVWSSPDML 60
Db 1 MGAPAAASLLILLLLFACCCWAPGAGNLSQD----- 29

QY 61 ASQDSQPTSDTETVAGGTVVLKQVKDHEDSSLOWSNPAQQTLYFGEKRALRDNRIOIV 120
Db 30 ---DSQPTSDTETVAGGTVVLKQVKDHEDSSLOWSNPAQQTLYFGEKRALRDNRIOIV 86

QY 121 TSTPHELSSISNVALADGEYTCSTFTWPTAKSLVTVLGIPOKPIITGYKSSLREKD 180
Db 87 TSTPHELSSISNVALADGEYTCSTFTWPTAKSLVTVLGIPOKPIITGYKSSLREKD 146

QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKPTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKPTVSSSVTFQVTRDDGAS 206

QY 241 IVCSVNHESLKGADRSSTORIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 300
Db 207 IVCSVNHESLKGADRSSTORIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 266

QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTGTATSNMGSKAYYTLNNDPSPVPSSS 360
Db 267 WEKEGVPPLKMTQESALIFPFLNKSDSGTGTATSNMGSKAYYTLNNDPSPVPSSS 326

QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHVLI RHKGYLT HEAKGSDDAPDADTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLLMILIFLGHVLI RHKGYLT HEAKGSDDAPDADTAIINAE 386

QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

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Search completed: May 27, 2004, 09:52:23
Job time : 38.7009 secs

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.8%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAALLLLLLLFFACCCWAPGAGNLSDQYWGQEDLELGLTAPLDEALISSTWSSPDM 60
DB 1 MGAPAAALLLLLLLFFACCCWAPGAGNLSDQ----- 29
QY 61 ASQDSQPTSDTETVAGGTVLKQVKDHDSSLOWNPAQOTLYFGKRALRDNRIQLV 120
DB 30 ---DSQPTSDTETVAGGTVLKQVKDHDSSLOWNPAQOTLYFGKRALRDNRIQLV 86
QY 121 TSTPHELISISNVALADGEYTCSTFTMPVTRAKSLVTLVGLPQKPIITGYKSSLRKD 180
DB 87 TSTPHELISISNVALADGEYTCSTFTMPVTRAKSLVTLVGLPQKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGFETRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGFETRIQEDPENGKTFVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKADRSSTORIEVLVPTAMIRDPDPHPPREGKLLHCEGRNPVPQVYL 300
DB 207 IVCSVNHESLKADRSSTORIEVLVPTAMIRDPDPHPPREGKLLHCEGRNPVPQVYL 266
QY 301 WEKGSVPLKWTQTSALIFPFLNKSDSTYCTATSNMGSKYKAYTLNNDPSPVPS 360
DB 267 WEKGSVPLKWTQTSALIFPFLNKSDSTYCTATSNMGSKYKAYTLNNDPSPVPS 326
QY 361 SYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGYLTHEAKGSDDAPDADTAIINAE 420
DB 327 SYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGYLTHEAKGSDDAPDADTAIINAE 386
QY 421 QSGGDDKEYFI 432
DB 387 QSGGDDKEYFI 398

US-09-907-841-84

RESULT 15
US-09-904-011-84
Sequence 84, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

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QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 13
US-09-824-84
; Sequence 84, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-84

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Loca. Similarity 92.1%; Pred. No. 5 se-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQEQDLELGLTAPLDEAISTVWSSPDML 60
Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQEQDLELGLTAPLDEAISTVWSSPDML 60
QY 61 ASQDSQPWTSDETVAGGTVVLKCOVKDHDSSLOWNSPAAQOTLYFGKKAALDRNRIQLV 120
Db 30 ---DSQPWTSDETVAGGTVVLKCOVKDHDSSLOWNSPAAQOTLYFGKKAALDRNRIQLV 86
QY 121 TSTPHELSSISNVALADEGEYTCSTFTWPTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELSSISNVALADEGEYTCSTFTWPTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDQELHGBPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKQDQELHGBPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRTSQRIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGADRTSQRIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNPVPQOYL 266
QY 301 WEKGVVPLKMTQESALIFPFINKSDSGTYGCTATSNMGSYKAYVTLNVNDFSPVSSS 360
Db 267 WEKGVVPLKMTQESALIFPFINKSDSGTYGCTATSNMGSYKAYVTLNVNDFSPVSSS 326
QY 361 SYTHAIIIGGIVAFIVFLLIMLIFLGHYLIIRKGYTLTHEAKGSDPADADTAIINAE 420
Db 327 SYTHAIIIGGIVAFIVFLLIMLIFLGHYLIIRKGYTLTHEAKGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 14
US-09-907-841-84
; Sequence 84, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

US-09-778-187B-10

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCCWAPGANLSODGYWQEQDLELGTAPLDEAISSTVWSSPDM 60
Db 1 MGAPAAASLLLLLLFACCCWAPGANLSOD----- 29
QY 61 ASQSQPWTSDETVVAGTIVLKCQVCKHEDSSLOWNPAQOTLYFGEKRALRDNRIOLV 120
Db 30 ---DSQPWTSDETVVAGTIVLKCQVCKHEDSSLOWNPAQOTLYFGEKRALRDNRIOLV 86
QY 121 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLVIGIPKPIITGYKSLREKD 180
Db 87 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLVIGIPKPIITGYKSLREKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGCKLLHCEGRGNVPVQOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGCKLLHCEGRGNVPVQOYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDPSPVPSSS 360
Db 267 WEKESVPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDPSPVPSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAINAEGG 420
Db 327 STYHAIIGGIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAINAEGG 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 12

US-09-902-853-84
; Sequence 84, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, A.
; APPLICANT: Gottsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCCWAPGANLSODGYWQEQDLELGTAPLDEAISSTVWSSPDM 60
Db 1 MGAPAAASLLLLLLFACCCWAPGANLSOD----- 29
QY 61 ASQSQPWTSDETVVAGTIVLKCQVCKHEDSSLOWNPAQOTLYFGEKRALRDNRIOLV 120
Db 30 ---DSQPWTSDETVVAGTIVLKCQVCKHEDSSLOWNPAQOTLYFGEKRALRDNRIOLV 86
QY 121 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLVIGIPKPIITGYKSLREKD 180
Db 87 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLVIGIPKPIITGYKSLREKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGCKLLHCEGRGNVPVQOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGCKLLHCEGRGNVPVQOYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDPSPVPSSS 360
Db 267 WEKESVPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDPSPVPSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAINAEGG 420
Db 327 STYHAIIGGIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAINAEGG 386

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-84

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEDLELGLTAPLDEAISSTVWSSPDML 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVVAGGTIVLKCQVKHEDSSLOWSNPAQOTLYFGEKRALRDNIQLV 120
DB 30 ---DSQPWTSDETVVAGGTIVLKCQVKHEDSSLOWSNPAQOTLYFGEKRALRDNIQLV 86
QY 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
DB 87 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKCTFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKCTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGRGNPVPQQYL 300
DB 207 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGRGNPVPQQYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTYLNVNDPSPVSSS 360
DB 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTYLNVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 420
DB 327 STYHAIIGGIVAFIVFLMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

RESULT 10
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEDLELGLTAPLDEAISSTVWSSPDML 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVVAGGTIVLKCQVKHEDSSLOWSNPAQOTLYFGEKRALRDNIQLV 120
DB 30 ---DSQPWTSDETVVAGGTIVLKCQVKHEDSSLOWSNPAQOTLYFGEKRALRDNIQLV 86
QY 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
DB 87 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKCTFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKCTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGRGNPVPQQYL 300
DB 207 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGRGNPVPQQYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTYLNVNDPSPVSSS 360
DB 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTYLNVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 420
DB 327 STYHAIIGGIVAFIVFLMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

RESULT 11
US-09-778-187B-10
; Sequence 10, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Farnlow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 398
; TYPE: PRT
; ORGANISM: homo sapiens

```

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; TYPE: PRT
; LENGTH: 398
; ORGANISM: Homo sapiens
US-09-909-088B-84

Query Match      90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.8%; Pred. No. 5.Se-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY      1  MGAPASLULLLLLFACCGWPGANLSQDGYWQEDLGLTAPLDEALSSVWSPDML 60
DB      1  MGAPASLULLLLLFACCGWPGANLSQD----- 29

QY      61  ASQDSQFWSDETVVAGGTVLKCVQKDHEDSSLOWNPAQQTLYFGEKRALDRNRIQJV 120
DB      30  ---DSQFWSDETVVAGGTVLKCVQKDHEDSSLOWNPAQQTLYFGEKRALDRNRIQJV 86

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QY      121  TSTPHELISISINVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
DB      87  TSTPHELISISINVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY      181  TATINCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNKGKTFVSSSVTFQVTRDDGAS 240
DB      147  TATINCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNKGKTFVSSSVTFQVTRDDGAS 206
QY      241  IVCSVNHESLKADRSQSRIEVLVYPTAMIRDPDPPHREGQKLLHCEGRGNPVPQOYL 300
DB      207  IVCSVNHESLKADRSQSRIEVLVYPTAMIRDPDPPHREGQKLLHCEGRGNPVPQOYL 266
QY      301  WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTYLNVNDSFVPSSS 360
DB      267  WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTYLNVNDSFVPSSS 326
QY      361  STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADATAIINAE 420
DB      327  STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADATAIINAE 386
QY      421  QSGGDDKKEYFI 432
DB      387  QSGGDDKKEYFI 398

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RESULT 9

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US-09-905-291A-84
; Sequence 84, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

```


Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 266
QY 301 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 360
Db 267 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDDDAPDADTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDDDAPDADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 7

US-09-909-320-84
; Sequence 84, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-84

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSODGYWQEODLELGTAPLDEAISSTVWSSPDML 60
Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQD----- 29

QY 61 ASQDSQFWSDETAVAGTIVLKCQVKHEDSSLOWNPAQOTLYFGEKRALDNRIOLV 120
Db 30 --DSQFWSDETAVAGTIVLKCQVKHEDSSLOWNPAQOTLYFGEKRALDNRIOLV 86

QY 121 TSTPHELISISNVALADEGEYTCISFTMPVTAKSALTIVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELISISNVALADEGEYTCISFTMPVTAKSALTIVLGIPOKPIITGYKSSLRKD 146

QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206

QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 266

QY 301 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 360
Db 267 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 326

QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDDDAPDADTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDDDAPDADTAIINAE 386

QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 8

US-09-909-088B-84
; Sequence 84, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
QY 241 IVCNVNHESLKGDRTSQRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
Db 241 IVCNVNHESLKGDRTSQRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTTLNVNDSPVPSSS 360
Db 301 WEKEGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTTLNVNDSPVPSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTAINAEGG 420
Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTAINAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 5
US-10-302-041-2
; Sequence 2, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-2

Query Match 100.0%; Score 2264; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAALLLLLLFACCCWAPGANLSQDGYWQEDLELGTAPLDEALISSTVWSSPDML 60
Db 1 MGAPAAALLLLLLFACCCWAPGANLSQDGYWQEDLELGTAPLDEALISSTVWSSPDML 60
QY 61 ASQDSQPWTSDETAVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRIOVLV 120
Db 61 ASQDSQPWTSDETAVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRIOVLV 120
QY 121 TSTPHELISISNVALADEGEYTCSTFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKD 180
Db 121 TSTPHELISISNVALADEGEYTCSTFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKD 180
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
QY 241 IVCNVNHESLKGDRTSQRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
Db 241 IVCNVNHESLKGDRTSQRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTTLNVNDSPVPSSS 360
Db 301 WEKEGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTTLNVNDSPVPSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTAINAEGG 420

Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTAINAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 6
US-09-745-763-102
; Sequence 102, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 219
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/745,763
; FILING DATE: 18-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-745-763-102

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAALLLLLLFACCCWAPGANLSQDGYWQEDLELGTAPLDEALISSTVWSSPDML 60
Db 1 MGAPAAALLLLLLFACCCWAPGANLSQD----- 29
QY 61 ASQDSQPWTSDETAVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRIOVLV 120
Db 30 ---DSQPWTSDETAVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRIOVLV 86
QY 121 TSTPHELISISNVALADEGEYTCSTFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELISISNVALADEGEYTCSTFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240

;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/049,373
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,875
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/049,374
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,917
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,949
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;; PRIOR FILING DATE: 1997-06-06
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;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/068,054
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,064
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,053
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/070,923
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/073,160
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,159
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,165
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/085,925
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,921
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,923
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,922
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/092,921
;; PRIOR FILING DATE: 1998-07-15
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1245
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 361
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-933-767-361

Query Match 100.0%; Score 2264; DB 10; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAFAASLLLLLFFACWAPGANLSQDGYWQEDLEGLTGLTAPLDEAISTVWSSPDL 60
DB 1 MGAFAASLLLLLFFACWAPGANLSQDGYWQEDLEGLTGLTAPLDEAISTVWSSPDL 60
QY 61 ASQDSQPWTSDETVVAGTIVLKQVVDHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120

DB 61 ASQDSQPWTSDETVVAGTIVLKQVVDHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
QY 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPKPIITGYKSLREKD 180
DB 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPKPIITGYKSLREKD 180
QY 131 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
DB 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGAADRSTQRIEVLVYTPAMIRPDPPHREGQKLLHCEGNGNVPQOYL 300
DB 241 IVCSVNHESLKGAADRSTQRIEVLVYTPAMIRPDPPHREGQKLLHCEGNGNVPQOYL 300
QY 301 WEKGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNDPSPVPS 360
DB 301 WEKGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNDPSPVPS 360
QY 361 STVHAIIGGIVAFIVFLLMLIFLGHYLRHKGTLYLTHKAGSDDDAPDADTAINAEGG 420
DB 361 STVHAIIGGIVAFIVFLLMLIFLGHYLRHKGTLYLTHKAGSDDDAPDADTAINAEGG 420
QY 421 QSGGDDKKYFI 432
DB 421 QSGGDDKKYFI 432

RESULT 4
US-10-161-572-49
;; Sequence 49, Application US/10161572
;; Publication No. US20030087266A1
;; GENERAL INFORMATION:
;; APPLICANT: EXELIXIS, INC.
;; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
;; FILE REFERENCE: EX02-097C-PC
;; CURRENT APPLICATION NUMBER: US/10/161,572
;; CURRENT FILING DATE: 2002-06-03
;; PRIOR APPLICATION NUMBER: US 60/296,076
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/328,605
;; PRIOR FILING DATE: 2001-10-10
;; PRIOR APPLICATION NUMBER: US 60/338,733
;; PRIOR FILING DATE: 2001-10-22
;; PRIOR APPLICATION NUMBER: US 60/357,253
;; PRIOR FILING DATE: 2002-02-15
;; PRIOR APPLICATION NUMBER: US 60/357,600
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 49
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-161-572-49

Query Match 100.0%; Score 2264; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAFAASLLLLLFFACWAPGANLSQDGYWQEDLEGLTGLTAPLDEAISTVWSSPDL 60
DB 1 MGAFAASLLLLLFFACWAPGANLSQDGYWQEDLEGLTGLTAPLDEAISTVWSSPDL 60
QY 61 ASQDSQPWTSDETVVAGTIVLKQVVDHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
DB 61 ASQDSQPWTSDETVVAGTIVLKQVVDHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
QY 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPKPIITGYKSLREKD 180
DB 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPKPIITGYKSLREKD 180
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240

QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRDPHPHREGQKLLHCEGRGNPVPQYL 300
Db 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRDPHPHREGQKLLHCEGRGNPVPQYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKYKAYTTLNVDSPVPSS 360
Db 301 WEKEGVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKYKAYTTLNVDSPVPSS 360
QY 361 STYHAIIGGIVAFIVFLLMLFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAEGG 420
Db 361 STYHAIIGGIVAFIVFLLMLFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 2
US-09-778-187b-8
; Sequence 8, Application US/09778187b
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187b
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 432
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187b-8

Query Match 100.0%; Score 2264; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLILLILLFACCAWAGGANLSODGYWQEOLELGTAPLDEAISSTVWSSPDM 60
Db 1 MGAPASLILLILLFACCAWAGGANLSODGYWQEOLELGTAPLDEAISSTVWSSPDM 60
QY 61 ASQDSQPWTSDETAVAGGTVLKCQVKHEDSLSWNSPAQOTLYFEGKRALRDNRILQ 120
Db 61 ASQDSQPWTSDETAVAGGTVLKCQVKHEDSLSWNSPAQOTLYFEGKRALRDNRILQ 120
QY 121 TSTPHELSSISGNVALADGEYTCSTFTMPVTRAKSLVTLVGIQPKPIITGYKSLREX 180
Db 121 TSTPHELSSISGNVALADGEYTCSTFTMPVTRAKSLVTLVGIQPKPIITGYKSLREX 180
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRDPHPHREGQKLLHCEGRGNPVPQYL 300
Db 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRDPHPHREGQKLLHCEGRGNPVPQYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKYKAYTTLNVDSPVPSS 360
Db 301 WEKEGVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKYKAYTTLNVDSPVPSS 360
QY 361 STYHAIIGGIVAFIVFLLMLFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAEGG 420

Db 361 STYHAIIGGIVAFIVFLLMLFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 3
US-09-933-767-361
; Sequence 361, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 36.7009 Seconds
(without alignments)

3286.999 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPASLLLLLLLLFACWA.....AIINAEQSGGGDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	432	9	US-09-778-510-2
2	2264	100.0	432	9	US-09-778-187B-8
3	2264	100.0	432	10	US-09-933-572-361
4	2264	100.0	432	14	US-10-161-572-49
5	2264	100.0	432	14	US-10-302-041-2
6	2059	90.9	398	9	US-09-745-763-102
7	2059	90.9	398	9	US-09-909-320-84
8	2059	90.9	398	9	US-09-909-088B-84
9	2059	90.9	398	9	US-09-905-291A-84
10	2059	90.9	398	9	US-09-778-510-6
11	2059	90.9	398	9	US-09-778-187B-10
12	2059	90.9	398	9	US-09-902-853-84
13	2059	90.9	398	9	US-09-907-824-84
14	2059	90.9	398	9	US-09-907-841-84
15	2059	90.9	398	10	US-09-904-011-84

16	2059	90.9	398	10	US-09-906-742-84	Sequence 84, Appl
17	2059	90.9	398	10	US-09-906-838-84	Sequence 84, Appl
18	2059	90.9	398	10	US-09-907-613-84	Sequence 84, Appl
19	2059	90.9	398	10	US-09-907-942-84	Sequence 84, Appl
20	2059	90.9	398	10	US-09-904-859-84	Sequence 84, Appl
21	2059	90.9	398	10	US-09-909-204-84	Sequence 84, Appl
22	2059	90.9	398	10	US-09-904-820-84	Sequence 84, Appl
23	2059	90.9	398	10	US-09-904-786-84	Sequence 84, Appl
24	2059	90.9	398	10	US-09-906-646-84	Sequence 84, Appl
25	2059	90.9	398	10	US-09-906-700-84	Sequence 84, Appl
26	2059	90.9	398	10	US-09-903-786-84	Sequence 84, Appl
27	2059	90.9	398	10	US-09-902-903-84	Sequence 84, Appl
28	2059	90.9	398	10	US-09-903-749A-84	Sequence 84, Appl
29	2059	90.9	398	10	US-09-904-119-84	Sequence 84, Appl
30	2059	90.9	398	10	US-09-904-956-84	Sequence 84, Appl
31	2059	90.9	398	10	US-09-902-736-84	Sequence 84, Appl
32	2059	90.9	398	10	US-09-907-794-84	Sequence 84, Appl
33	2059	90.9	398	10	US-09-903-943-84	Sequence 84, Appl
34	2059	90.9	398	10	US-09-903-462-84	Sequence 84, Appl
35	2059	90.9	398	10	US-09-907-925-84	Sequence 84, Appl
36	2059	90.9	398	10	US-09-902-632-84	Sequence 84, Appl
37	2059	90.9	398	10	US-09-903-520-84	Sequence 84, Appl
38	2059	90.9	398	10	US-09-905-056-84	Sequence 84, Appl
39	2059	90.9	398	10	US-09-909-064-84	Sequence 84, Appl
40	2059	90.9	398	10	US-09-904-553-84	Sequence 84, Appl
41	2059	90.9	398	10	US-09-905-381-84	Sequence 84, Appl
42	2059	90.9	398	10	US-09-905-088-84	Sequence 84, Appl
43	2059	90.9	398	10	US-09-907-575-84	Sequence 84, Appl
44	2059	90.9	398	10	US-09-905-075-84	Sequence 84, Appl
45	2059	90.9	398	10	US-09-902-759-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match 100.0%; Score 2264; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGAPASLLLLLLLLFACWA	PGGANLSDGWQEO	DLGLTAPLDEA	ISSTVWSSPDL 60
Db	1	MGAPASLLLLLLLLFACWA	PGGANLSDGWQEO	DLGLTAPLDEA	ISSTVWSSPDL 60
Qy	61	ASQDSQPWTSDET	VAGGT	VVLKCVKDHED	SSLOWNPAQQTLYFGKRALRDNRIQLV 120
Db	61	ASQDSQPWTSDET	VAGGT	VVLKCVKDHED	SSLOWNPAQQTLYFGKRALRDNRIQLV 120
Qy	121	TSTPHEL	SISIN	VALADEGYTCS	IFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db	121	TSTPHEL	SISIN	VALADEGYTCS	IFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180

Job time : 52.4442 secs

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21417.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 348; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PENCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 398 AA;
Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 3.5e-148;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAALLLLLLFACCAWAGANLSQDGYVQEQDLELGTILAPLDEAISITVWSSPDM 60
DB 1 MGAPAAALLLLLLFACCAWAGANLSQD----- 29
QY 61 ASQDSQPWTSDET VVAGT VVLKCVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 120
DB 30 ---DSQPWTSDET VVAGT VVLKCVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 86
QY 121 TSTPHELSISISNVALADEGETCSIFTPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
DB 87 TSTPHELSISISNVALADEGETCSIFTPVRTAKSLVTVLGIPOKPIITGYKSLREKD 146
QY 181 TATLNCQSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMTRPDPHPHREGQKLLHCEGRGNVPQOYL 300
DB 207 IVCSVNHESLKGADRSQRIEVLVYTPAMTRPDPHPHREGQKLLHCEGRGNVPQOYL 266
QY 301 WEKEGSPPLKWTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYYTLNVNDSPVPSSS 360
DB 267 WEKEGSPPLKWTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYYTLNVNDSPVPSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTAEAKGSDADPADTAIINAE 420
DB 327 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTAEAKGSDADPADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

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PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX XX
XX (GETH ) GENENTECH INC.
XX XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2001-081051/09.
XX N-PSDB; AAF72387.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
XX disease).
XX
XX Claim 1; Fig 32; 393pp; English.
XX
XX The present sequence is one of sixty one novel secreted and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful for treating skin
XX diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
XX gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
XX diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
XX cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
XX ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
XX disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
XX infertility, AIDS and diabetes and retinal disorders such as retinitis
XX pigmentosa. The PRO nucleic acids have applications in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping
XX
XX Sequence 398 AA;
XX
XX Query Match 90.9%; Score 2059; DB 4; Length 398;
XX Best Local Similarity 92.1%; Pred. No. 3.5e-148;
XX Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
XX
XX 1 MGAPASLLLLLLFACCMAGGAGNLSQDGVWQDLELGTAPLDEAISSTVWSSPDML 60
XX 1 MGAPASLLLLLLFACCMAGGAGNLSQD-----29
XX
XX 61 ASODSQPWTSDETVAGGTVLKQVQKDHEDSLQWNPAAQOTLYFGKEKALRDNRILV 120
XX 30 ---DSQPWTSDETVAGGTVLKQVQKDHEDSLQWNPAAQOTLYFGKEKALRDNRILV 86
XX
XX 121 TSTPHELISISNVALADEGYTCSTFTMPVTKASLTVLGIPOKPIITGYKSSIREKD 180
XX 87 TSTPHELISISNVALADEGYTCSTFTMPVTKASLTVLGIPOKPIITGYKSSIREKD 146
XX
XX 181 TATLNCSSGSKPAARLTWRKGQDLHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
XX 147 TATLNCSSGSKPAARLTWRKGQDLHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
XX
XX 241 IVCSNVHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVQYVL 300
XX 207 IVCSNVHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVQYVL 266
XX
XX 301 WEKEGVPPLKMTQESALIPFPLINKSDSGYTGCTATSNMGSKYKAYTYLNVNDFSPVSS 360
XX 267 WEKEGVPPLKMTQESALIPFPLINKSDSGYTGCTATSNMGSKYKAYTYLNVNDFSPVSS 326
XX
XX 361 STVHAIIGGVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTALINAEKG 420
XX 327 STVHAIIGGVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTALINAEKG 386

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QY 421 QSGGDDKKEYFI 432
Db 337 QSGGDDKKEYFI 398
RESULT 15
AAU12345
ID AAU12345 standard; protein; 398 AA.
XX
XX AAU12345;
AC AAU12345;
XX
XX 24-OCT-2001 (first entry)
DT
XX Human PRO258 polypeptide sequence.
DE
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; factor VIIA; gene therapy.
XX Homo sapiens.
OS
XX WO200140466-A2.
PN
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032678.
XX
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 03-DEC-1999; 99US-0170262P.
XX 16-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 03-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 01-MAR-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005601.
XX 03-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000US-0187202P.
XX 15-MAR-2000; 2000WO-US006319.
XX 20-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000WO-US007377.
XX 30-MAR-2000; 2000WO-US007532.
XX 17-MAY-2000; 2000WO-US008439.
XX 22-MAY-2000; 2000WO-US013705.
XX 30-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US014941.
XX 05-JUN-2000; 2000WO-US015264.
XX 28-JUL-2000; 2000US-0209832P.
XX 11-AUG-2000; 2000WO-US020710.
XX 23-AUG-2000; 2000WO-US022031.
XX 24-AUG-2000; 2000WO-US023522.
XX 08-NOV-2000; 2000WO-US023328.
XX 10-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX

```

XX	SQ	Sequence 398 AA;	
		Query Match	90.9%; Score 2059; DB 3; Length 398;
		Best Local Similarity	92.11%; Pred. No. 3.5e-148;
		Matches 398; Conservative	0; Mismatches 0; Indels 34; Gaps 1
QY	1	MGAPAAASLLLLLLFACCAWPGGANLSQDGVQWQDLELGLTAPLDEAISTTWSSPDML 60	
DB	1	MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29	
QY	61	ASQDSQPWTSDETVAAGTIVVLKQVKDHDSSLSQNSNPAQQTLYFGCKRALRDNRIQLV 120	
DB	30	----DSQPWTSDETVAAGTIVVLKQVKDHDSSLSQNSNPAQQTLYFGCKRALRDNRIQLV 86	
QY	121	TSTPHELISISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGVKSSIREKD 180	
DB	87	TSTPHELISISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGVKSSIREKD 146	
QY	181	TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRREDDGAS 240	
DB	147	TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRREDDGAS 206	
QY	241	IVCSVNNHESLKGADRSQSRIEVLVYPTAMIRDPDPHPREGQKLLHLCRGRGNPVPQYL 300	
DB	207	IVCSVNNHESLKGADRSQSRIEVLVYPTAMIRDPDPHPREGQKLLHLCRGRGNPVPQYL 266	
QY	301	MEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYAYTLNVNDPSPVPSSS 360	
DB	267	MEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYAYTLNVNDPSPVPSSS 326	
QY	361	STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTVLTHKGSDDAPADTAIINAEGG 420	
DB	327	STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTVLTHKGSDDAPADTAIINAEGG 386	
QY	421	QSGGDDKKEYFI 432	
DB	387	QSGGDDKKEYFI 398	
RESULT 14			
AAB80226		ID AAB80226 standard; protein; 398 AA.	
XX	AC	AAB80226;	
XX	XX		
DT	24-APR-2001	(first entry)	
XX	XX	Human PRO258 protein.	
DE	DE	Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;	
KW	KW	anti-parkinsonian neurotropic; neuroprotective; vulnerary; cardiant;	
KW	KW	antiangiogenic; vasotropic; antiasthmatic; antineumatic; cancer;	
KW	KW	antiarthritic; antinfertility; antididiabetic; antiviral; diabetes;	
KW	KW	ophthalmological; gene therapy; skin disease; gastrointestinal disorder;	
XX	XX	ischaemia; inflammation.	
XX	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200104311-A1.	
FD	FD	18-JAN-2001.	
XX	XX		
XX	XX	22-FEB-2000; 2000WO-US004414.	
PR	PR	07-JUL-1999; 99US-0143048P.	
PR	PR	26-JUL-1999; 99US-0145698P.	
PR	PR	28-JUL-1999; 99US-0146222P.	
PR	PR	08-SEP-1999; 99WO-US020594.	
PR	PR	13-SEP-1999; 99WO-US020944.	
PR	PR	15-SEP-1999; 99WO-US021090.	
PR	PR	15-SEP-1999; 99WO-US021547.	
PR	PR	25-OCT-1999; 99WO-US021547.	

PT Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 PT costimulatory molecules for therapeutics against infections, autoimmune
 XX diseases and inflammation.
 XX
 PS Claim 8; Page 47-48; 57pp; English.
 XX
 CC The present sequence represents the short extracellular form of human B7-
 CC 1 (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine
 CC production, cell proliferation, and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the disordered mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting
 CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic
 CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes
 CC which catalyze a colorimetric or fluorometric reaction, may be attached
 CC to a B7L-1 polypeptide, e.g. nitrogen mustards are attached to the B7L-1
 CC and used to treat various forms of cancer
 XX
 SQ Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 3; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQBDLEGLTGLAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQBDLEGLTGLAPLDEAISTVWSSPDML 29
 QY 61 ASQDSQPWTSDETAVAGTTLKCVKDHEDSSLOWSNPAQOTLYFGKRALDNRILQV 120
 Db 30 ---DSQPWTSDETAVAGTTLKCVKDHEDSSLOWSNPAQOTLYFGKRALDNRILQV 86
 QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLGIPQKPIITGYKSSIREKD 180
 Db 87 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLGIPQKPIITGYKSSIREKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQYVL 300
 Db 207 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQYVL 266
 QY 301 WEKEGVPPLKMTQESALIPFPFLKSDSGTYGCTATSNMGSKYAYTLNVNDSPSPSS 360
 Db 267 WEKEGVPPLKMTQESALIPFPFLKSDSGTYGCTATSNMGSKYAYTLNVNDSPSPSS 326
 QY 361 STYHAIIGGVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADTAIINAEAG 420
 Db 327 STYHAIIGGVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADTAIINAEAG 386
 QY 421 QSGGDDKKEYFI 432
 Db 387 QSGGDDKKEYFI 398

RESULT 12

AAV45095

ID AAY45095 standard; protein; 398 AA.

XX AAY45095;

AC AAY45095;

XX

DT 31-MAY-2000 (first entry)
 XX
 DE Human LDCAM binding protein, B7L-1 short form.
 KW
 KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-L1;
 KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
 KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.
 XX
 OS Homo sapiens.
 XX
 FN WO200008158-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 05-AUG-1999; 99WO-US017905.
 XX
 PR 07-AUG-1998; 98US-0095672P.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Baum PR, Fanslow WC;
 PI
 XX WPI; 2000-205712/18.
 DR
 DR N-PSDB; AAZ50887.
 XX
 PT Novel molecules designated LDCAM are capable of altering or modulating T
 PT cell function.
 XX
 XX Disclosure; Page 53-54; 44pp; English.

The present amino acid sequence is the human LDCAM (lymphoid derived
 dendritic cell adhesion molecule) binding protein, B7L-1 short form. B7L
 -1 has sequence similarity to adhesion molecule, B7-1. B7L-1 and LDCAM
 display homology within their intracellular domain, found on many of the
 same cell types and their cell-bound forms deliver similar signals when
 engaged and are termed as co-receptors or counter structures. LDCAM
 polypeptides interacts with T cell surface molecules to alter signalling
 and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM
 binding protein and increases natural killer (NK) cell populations. It
 may be used to measure the biological activity and as quality control
 reagents of LDCAM binding proteins. LDCAM may be used for treating
 disorders associated with malfunctioning of immune system, inflammation,
 autoimmune disorders, viral infected cells, infectious diseases and for
 killing tumour cells. They are also useful for prevention or reducing the
 effect of organ and bone marrow transplant rejection and for modulating T
 cell immune responses. LDCAM polypeptides may also be used as carriers
 for delivering agents attached to T cells or cells bearing B7L-1

Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 3; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQBDLEGLTGLAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQBDLEGLTGLAPLDEAISTVWSSPDML 29
 QY 61 ASQDSQPWTSDETAVAGTTLKCVKDHEDSSLOWSNPAQOTLYFGKRALDNRILQV 120
 Db 30 ---DSQPWTSDETAVAGTTLKCVKDHEDSSLOWSNPAQOTLYFGKRALDNRILQV 86
 QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLGIPQKPIITGYKSSIREKD 180
 Db 87 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLGIPQKPIITGYKSSIREKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQYVL 300

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Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYLTTHKAGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 10
ID AAY94403 standard; protein; 398 AA.
AC AAY94403;
XX 11-SEP-2000 (first entry)
XX Human ACAM cellular adhesion molecule encoded by cDNA clone ACAM#4.
DE Human; cellular adhesion molecule; ACAM; nontropic; antiepileptic;
KW neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
KW dementia; epilepsy; schizophrenia; peripheral nerve injury;
KW diabetic neuropathy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..398
FT /label= ACAM
PN WO2000032633-A1.
XX 08-JUN-2000.
XX 02-DEC-1999; 99WO-US028878.
XX 02-DEC-1998; 98US-00203462.
XX (ICOS-) ICOS CORP.
XX Hoekstra DM, Loughney K, Staunton DE, Vazeux R;
DR WPI; 2000-422952/36.
DR N-PSDB; AAY94403.
XX Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
PT for diagnosing, preventing and treating diseases associated with ACAM
PT expression and activity, e.g. epilepsy and schizophrenia.
XX Claim 5; Page 149-150; 187pp; English.
XX The present sequence is a novel adhesion molecule, designated ACAM. The
CC full-length nucleotide sequence was identified in clone ACAM#4 of a human
CC foetal brain library. The polypeptide is 100% homologous to the
CC polypeptide encoded by clone ACAM#5 (AAA30423) from the same library
CC except that it contains a 34 amino acid deletion. It is believed to
CC correspond to an alternative form of ACAM. The nucleotide sequence and
CC the protein it encodes may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate ACAM expression and
CC activity such as dementia, epilepsy, schizophrenia, peripheral nerve
CC injuries and diabetic neuropathies. They may be used to rectify mutations
CC or deletions in a patient's genome that affect the activity of ACAM or to
CC supplement insufficient ACAM production in a patient. The nucleotide
CC sequence may be integrated into an expression vector and inserted into a
CC host cell for protein expression in vitro or in vivo. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate
CC ACAM expression. The nucleotide sequence may also be used as a DNA probe
CC in diagnostic assays (e.g. PCR) to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and hence determine which
CC patients may be in need of restorative therapy. ACAM polypeptides may be
CC used as antigens in the production of antibodies against ACAM and in
CC assays to identify modulators (agonists and antagonists) of ACAM

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CC expression and activity
XX Sequence 398 AA;
SQ
Query Match 90.9%; Score 2059; DB 3; Length 398;
Best Local Similarity 92.1%; Pred. No. 3.5e-148;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLILLLIFACCNAPGGANLSQDSYQWQOELELGLTAPLDEAISSTWSSPDM 60
Db 1 MGAPAAASLILLLIFACCNAPGGANLSQDSYQWQOELELGLTAPLDEAISSTWSSPDM 60
QY 61 ASQDSQPTSDETWAGGTWLVKQVKDHEDSLQNSNPAQOTLYFGEKRALDNRILQV 120
Db 30 ---DSQPTSDETWAGGTWLVKQVKDHEDSLQNSNPAQOTLYFGEKRALDNRILQV 86
QY 121 TSTPHELSSISNVALADEGEYTCSTFTMPRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELSSISNVALADEGEYTCSTFTMPRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRTSQRIVLYTPTAMIRDPDPHREGOKLLHCEGRGNPVQOYL 300
Db 207 IVCSVNHESLKGADRTSQRIVLYTPTAMIRDPDPHREGOKLLHCEGRGNPVQOYL 266
QY 301 WEKEGSVPFLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDSPSPVSS 360
Db 267 WEKEGSVPFLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDSPSPVSS 326
QY 361 SYTHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYLTTHKAGSDPADADTAIINAE 420
Db 327 SYTHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYLTTHKAGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 11
AAY69288
ID AAY69288 standard; protein; 398 AA.
XX
AC AAY69288;
XX
DT 19-JUN-2000 (first entry)
XX
DE Amino acid sequence of extracellular form of human B7-1 (CD80).
XX
KW Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
KW CD28; CTLA4; T cell surface receptor; cytokine production;
KW cell proliferation; T cell; infection; autoimmune disease; inflammation;
XX quality assurance; cancer.
XX Homo sapiens.
XX WO200003057-A2.
XX 17-FEB-2000.
XX 05-AUG-1999; 99WO-US017906.
XX 07-AUG-1998; 98US-0095663P.
XX (IMV) IMMUNEX CORP.
XX Baum PR;
XX WPI; 2000-205674/18.
XX N-PSDB; AAZ61418.
XX

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QY 421 QSGGDKKEYFI 432
 Db 387 QSGGDKKEYFI 398
 RESULT 9
 ID AAY13358 standard; protein; 398 AA.
 XX AAY13358;
 AC
 DT 25-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of protein PRO258.
 XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophica areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 PN W09914328-A2.
 XX
 PD 25-MAR-1999.
 XX
 FF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 18-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.

21-NOV-1997; 97US-0066120P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 25-NOV-1997; 97US-0066840P.
 XX (GETH) GENENTECH INC.
 XX
 FI Wood WZ, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 XX
 DR WPI; 1999-229533/19.
 DR N-PSDB; AAX52229.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT Gastrointestinal ulceration.
 XX
 PS Claim 12; Fig 32; 320pp; English.
 XX
 CC AAY13344-403 represent secreted and transmembrane human proteins. The
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophica areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX
 SQ Sequence 398 AA;
 Query Match 90.9%; Score 2059; DB 2; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAASLLLLLLLLFACCCWAPGGANLSQDGYWQEQDLELGLTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLLLFACCCWAPGGANLSQD----- 29
 QY 61 ASQDSQPWTSDETVVAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGEKRALDRNIQIV 120
 Db 30 ---DSQPWTSDETVVAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGEKRALDRNIQIV 86
 QY 121 TSTPHELSTISINVALADGEYTCSTFTMPVETAKSLVTLGIPKPIITGVKSSIREKD 180
 Db 87 TSTPHELSTISINVALADGEYTCSTFTMPVETAKSLVTLGIPKPIITGVKSSIREKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
 QY 241 IVCSVNHESLKADSTSORLEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPQOYL 300
 Db 207 IVCSVNHESLKADSTSORLEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPQOYL 266
 QY 301 WEKGSVPPLKMTQBSALIFPFLNKS DSGTGTATSNMGSKYATYTLNVNDPSVPSSS 360
 Db 267 WEKGSVPPLKMTQBSALIFPFLNKS DSGTGTATSNMGSKYATYTLNVNDPSVPSSS 326
 QY 361 STYHAIIGGIVAFVFLLLIMLIFLGHYLRHKGTLYLTHAKGSDPADPADTAIINAE 420

QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREKD 180
 DB 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREKD 180
 QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
 DB 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
 QY 241 IVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNVPVPOYL 300
 DB 241 IVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNVPVPOYL 300
 QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 DB 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 QY 361 STYHAIIGGIVAFIVFLLLMFLHGHYLIIRHKGTYLTHEAKGSDDDAPDADTAIINAE 420
 DB 361 STYHAIIGGIVAFIVFLLLMFLHGHYLIIRHKGTYLTHEAKGSDDDAPDADTAIINAE 420
 QY 421 QSGGDDKKEYFI 432
 DB 421 QSGGDDKKEYFI 432

RESULT 6
 AA53272 ID AAY53272 standard; protein; 433 AA.
 XX AC AAY53272;
 XX 21-JUL-2000 (first entry)
 DE Human Beat-like 1 (BL1) protein sequence.
 XX Human; Beat-like 1; BL1; nervous system.
 OS Homo sapiens.
 XX CN1242376-A.
 XX 26-JAN-2000.
 XX 27-JUL-1999; 99CN-00111018.
 XX 27-JUL-1999; 99CN-00111018.
 XX (BASI-) BASIC MEDICAL SCI RES INST CHINESE ACAD.
 PI Zhang B, Yuan J, Zhou Y;
 XX WPI; 2000-340013/30.
 DR N-PSDB; AAA13653.
 XX Human gene expressed in nerve tissue for studying tissue function.
 PS Disclosure; Fig 2; 14pp; Chinese.
 XX The present invention relates to a new specific expression gene, Beat-like 1 (BL1), from the human nervous system. BL1 is a nervous adhesion molecule and its specific expression can possess important action in maintenance of physiological function of the nervous system and pathogenic processes of some nervous system diseases. The present sequence represents the human BL1 given in the present invention

Query Match 99.5%; Score 2253.5; DB 3; Length 433;
 Best Local Similarity 99.8%; Pred. No. 6.2e-163;
 Matches 432; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MGAAPASLLLLLLFACCAWAPGANLSQGYWQEDLELGTALPLDRAISSTVWSSPDML 60
 |||||

DB 1 MGAAPASLLLLLLFACCAWAPGANLSQGYWQEDLELGTALPLDRAISSTVWSSPDML 60
 QY 61 ASQDSQFMTSDETVVAGTTLVKQVKDHEDSSLOWNPAQOTLYFGEKALDRNRIQLV 120
 DB 61 ASQDSQFMTSDETVVAGTTLVKQVKDHEDSSLOWNPAQOTLYFGEKALDRNRIQLV 120
 QY 121 TSTPHELISISINVALAD-EGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREK 179
 DB 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREK 180
 QY 180 DTATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGA 239
 DB 181 DTATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGA 240
 QY 240 SIVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNVPVPOY 299
 DB 241 SIVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNVPVPOY 300
 QY 300 LWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 359
 DB 301 LWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 QY 360 SSTDYHAIIGGIVAFIVFLLLMFLHGHYLIIRHKGTYLTHEAKGSDDDAPDADTAIINAE 419
 DB 361 SSTDYHAIIGGIVAFIVFLLLMFLHGHYLIIRHKGTYLTHEAKGSDDDAPDADTAIINAE 420
 QY 420 QSGGDDKKEYFI 432
 DB 421 QSGGDDKKEYFI 433

RESULT 7
 AAW80405 ID AAW80405 standard; protein; 398 AA.
 XX AC AAW80405;
 XX 25-MAR-2003 (revised)
 DT 13-JAN-1999 (first entry)
 XX A secreted protein encoded by clone crll62_25.
 DE Secreted protein; immune stimulating; suppressing;
 KW haematopoiesis regulating activity; tissue growth activity; activin;
 KW inhibin activity; chemotactic; chemokinetic activity; haemostatic;
 KW thrombolytic activity; anti-inflammatory activity; cadherin;
 KW tumour invasion suppressor activity; tumour inhibition activity.
 XX Homo sapiens.
 OS WO9844113-A1.
 XX 08-OCT-1998.
 XX 27-MAR-1998; 98WO-US006176.
 XX 28-MAR-1997; 97US-00823330.
 PR 25-MAR-1998; 98US-00047661.
 XX (GEMY) GENETICS INST INC.
 XX Jacobs K, McCoey JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX WPI: 1998-542703/46.
 DR N-PSDB; AAV63189.
 XX New isolated polynucleotide(s) and secreted proteins - are obtained from human cDNA libraries prepared from adult testes, foetal brain, adult brain, adult blood and placenta.
 PT Claim 13; Page 70-71; 124pp; English.

XX NI J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kwaw H, Fischer CL, Ferrie AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z;
 PI Greene JM;
 XX WPI; 2001-625724/72.
 DR N-PSDB; ABA83306.
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 XX Claim 11; Page 1142-1143; 1533pp; English.
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention

SQ Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 4; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDM 60
 DB 1 MGAPASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDM 60
 QY 61 ASQDSQPWTSDETVAAGTGVVLCQVQKHEDSSLOWNPAAQOTLYFGEKRALRNRIO 120
 DB 61 ASQDSQPWTSDETVAAGTGVVLCQVQKHEDSSLOWNPAAQOTLYFGEKRALRNRIO 120
 QY 121 TSTPHELSISINVALADEGEYTCISITMPVRTAKSLTVVLGIPQKPIITGYKSSIREKD 180
 DB 121 TSTPHELSISINVALADEGEYTCISITMPVRTAKSLTVVLGIPQKPIITGYKSSIREKD 180
 QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIOEDPNGKFTVSSVTVQVTRDDGAS 240
 DB 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIOEDPNGKFTVSSVTVQVTRDDGAS 240
 QY 241 IVCSVNHESLKGDRSTQRIEVLVYTPMTTRPPHPRGQKLLHCEGRGNVPQOYL 300
 DB 241 IVCSVNHESLKGDRSTQRIEVLVYTPMTTRPPHPRGQKLLHCEGRGNVPQOYL 300
 QY 301 WEKESGVPPLKMTQESALIFPFLNKSQSGTVGCTATSNMGSYKAYTYTLNVNDSPVPSS 360
 DB 301 WEKESGVPPLKMTQESALIFPFLNKSQSGTVGCTATSNMGSYKAYTYTLNVNDSPVPSS 360
 QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYYLTHAKGSDPADPADTAIINAE 420
 DB 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYYLTHAKGSDPADPADTAIINAE 420
 QY 421 QSGGDDKKEYFI 432
 |||||

Db 421 QSGGDDKKEYFI 432
 RESULT 5
 ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 ID ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 XX AC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 XX AC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 DT 13-AUG-2003 (first entry)
 XX Human IG gene related protein SEQ ID No 49.
 DE Breast cancer; p53 pathway modulating agent; IG; colon cancer;
 XX kidney cancer; lung cancer; ovary cancer; human.
 KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
 KW kidney cancer; lung cancer; ovary cancer; human.
 OS Homo sapiens.
 XX WO2002029040-A2.
 XX 12-DEC-2002.
 XX 03-JUN-2002; 2002WO-US017313.
 XX 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 22-OCT-2001; 2001US-0338733P.
 PR 15-FEB-2002; 2002US-0357253P.
 PR 15-FEB-2002; 2002US-0357600P.
 XX (EXEL-) EXELIXIS INC.
 PA Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI Lioubin MN;
 XX WPI; 2003-148660/14.
 XX Identifying a candidate p53 pathway modulators that are useful as targets
 PT for therapeutics or for diagnosing cancers associated with defective p53
 PT function, by providing an assay system having a purified IG polypeptide
 PT or nucleic acid.
 XX Claim 13; Page 214-216; 248pp; English.
 PS The invention relates to a novel method for identifying a candidate p53
 CC pathway modulating agent. The method comprises providing an assay system
 CC having a purified IG polypeptide or nucleic acid, or their functionally
 CC active fragment or derivative. The method is useful for identifying
 CC modulators of the p53 pathway, particularly for identifying agents for
 CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
 CC cancer or cancer of the ovary) associated with defective p53 function.
 CC The identified modulators are useful as targets for novel therapeutics.
 CC The method is also useful for diagnosing disorders associated with
 CC defective p53 function. The IG proteins or nucleic acids are useful as
 CC modifiers of the p53 pathway, and as therapeutic targets for disorders
 CC associated with defective p53 function. This sequence represents a human
 CC protein relating to the human IG genes used in the assay for identifying
 CC modulators of the p53 pathway of the invention
 XX SQ Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 6; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDM 60
 DB 1 MGAPASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDM 60
 QY 61 ASQDSQPWTSDETVAAGTGVVLCQVQKHEDSSLOWNPAAQOTLYFGEKRALRNRIO 120
 DB 61 ASQDSQPWTSDETVAAGTGVVLCQVQKHEDSSLOWNPAAQOTLYFGEKRALRNRIO 120

Db 241 IVCSVNHESLKGADRSQSRLEVIYPTAMIRPPPHREGQKLLHCEGRGNFVPOOYL 300
Qy 301 WEKEGSPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Db 301 WEKEGSPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Qy 361 STYHAIIGGIIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Db 361 STYHAIIGGIIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Qy 421 QSGGDDKXEYFI 432
Db 421 QSGGDDKXEYFI 432

RESULT 3
AAY45094
ID AAY45094 standard; protein; 432 AA.
XX AC AAY45094;
XX DT 31-MAY-2000 (first entry)
XX DE Human LDCAM binding protein, B7L-1 long form.
XX KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KW biological activity; quality control reagent; treatment; inflammation;
KW immune system disorder; autoimmune; viral infection; infectious disease;
KW organ transplant rejection; bone marrow; modulator; immune response.
XX OS Homo sapiens.
XX PN WO200008158-A2.
XX PD 17-FEB-2000.
XX PF 05-AUG-1999; 99WO-US017905.
XX PR 07-AUG-1998; 98US-0095672P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC;
XX DR WPI; 2000-205712/18.
XX DR N-PSDB; AAZ50886.
XX PS Novel molecules designated LDCAM are capable of altering or modulating T cell function.
XX FS Disclosure; Page 50-51; 44pp; English.
XX CC The present amino acid sequence is the human LDCAM (lymphoid derived dendritic cell adhesion molecule) binding protein, B7L-1 long form. B7L-1 has sequence similarity to adhesion molecule, B7-1. B7L-1 and LDCAM display homology within their intracellular domain, found on many of the same cell types and their cell-bound forms deliver similar signals when engaged and are termed as co-receptors or counter structures. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1

Query Match 100.0%; Score 2264; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No 9,9e-164; Indels 0; Gaps 0;
Matches 432; Conservative 0; Mismatches 0;
Qy 1 MGAPAAALLLLFACCAWPGGANLSQDGYWQDLELGTALFLDEAISSTVSSPDML 60
Db 1 MGAPAAALLLLFACCAWPGGANLSQDGYWQDLELGTALFLDEAISSTVSSPDML 60
Qy 61 ASQDSQPTSDETVAGTIVLKCQVXDHEDSSLOWNPAAQOTLYFGEKRALRNRQLV 120
Db 61 ASQDSQPTSDETVAGTIVLKCQVXDHEDSSLOWNPAAQOTLYFGEKRALRNRQLV 120
Qy 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLEKD 180
Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLEKD 180
Qy 181 TATLNCOSGSKPAARLTWRKQDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 181 TATLNCOSGSKPAARLTWRKQDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Qy 241 IVCSVNHESLKGADRSQSRLEVIYPTAMIRPPPHREGQKLLHCEGRGNFVPOOYL 300
Db 241 IVCSVNHESLKGADRSQSRLEVIYPTAMIRPPPHREGQKLLHCEGRGNFVPOOYL 300
Qy 301 WEKEGSPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Db 301 WEKEGSPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Qy 361 STYHAIIGGIIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Db 361 STYHAIIGGIIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Qy 421 QSGGDDKXEYFI 432
Db 421 QSGGDDKXEYFI 432

RESULT 4
ABB50413
ID ABB50413 standard; protein; 432 AA.
XX AC ABB50413;
XX DT 07-FEB-2002 (first entry)
XX DE Human secreted protein encoded by gene 113 SEQ ID NO:361.
XX KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
KW cytotatic; cardiant; vascular; anti-angiogenic; ophthalmological;
KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnary;
KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
KW neurological disorder; Huntington's chorea; Alzheimer's disease;
KW Parkinson's disease; infectious disease; chromosome 1.
XX OS Homo sapiens.
XX PN WO200162891-A2.
XX PD 30-AUG-2001.
XX PF 21-FEB-2001; 2001WO-US005614.
XX PR 24-FEB-2000; 2000US-0184836P.
XX PR 29-MAR-2000; 2000US-0193170P.
XX PA (HUMA-) HUMAN GENOME SCI INC.

CC dementia, epilepsy, schizophrenia, peripheral nerve injuries and diabetic
 CC neuropathies. They may be used to rectify mutations or deletions in a
 CC patient's genome that affect the activity of ACAM or to supplement
 CC insufficient ACAM production in a patient. The nucleotide sequence may be
 CC integrated into an expression vector and inserted into a host cell for
 CC protein expression in vitro or in vivo. Conversely, antisense nucleic
 CC acid molecules may be administered to down-regulate ACAM expression. The
 CC nucleotide sequence may also be used as a DNA probe in diagnostic assays
 CC (e.g. PCR) to detect and quantitate the presence of similar nucleic acid
 CC sequences in samples, and hence determine which patients may be in need
 CC of restorative therapy. ACAM polypeptides may be used as antigens in the
 CC production of antibodies against ACAM and in assays to identify
 CC modulators (agonists and antagonists) of ACAM expression and activity
 XX
 XX Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 3; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 QY 61 ASQDSQPWTSDETVAAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGKRALDRNRIOIV 120
 Db 61 ASQDSQPWTSDETVAAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGKRALDRNRIOIV 120
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 QY 181 TATLNCQSSGSKPAARLTWRKGDDELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
 Db 181 TATLNCQSSGSKPAARLTWRKGDDELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
 QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPREGQKLLHCEGRGNVPVQOYL 300
 Db 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPREGQKLLHCEGRGNVPVQOYL 300
 QY 301 WEKEGVPPLKMTQESALIPFLLNKSDSGYTGCTATSNMGSYKAYITLVNNDSPVPSSS 360
 Db 301 WEKEGVPPLKMTQESALIPFLLNKSDSGYTGCTATSNMGSYKAYITLVNNDSPVPSSS 360
 QY 361 STYHAIIGGIVATIVFLMLIFLGHYLRHKGTYLTHEAKGSDDAPADTAIINAEKG 420
 Db 361 STYHAIIGGIVATIVFLMLIFLGHYLRHKGTYLTHEAKGSDDAPADTAIINAEKG 420
 QY 421 QSGGDDKKEYFI 432
 Db 421 QSGGDDKKEYFI 432

RESULT 2

AA169286
 ID AAY69286 standard; protein; 432 AA.
 XX
 AC AAY69286;
 DT
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of long extracellular form of human B7-1 (CD80).
 XX
 KW Long form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
 KW CD28; CTLA4; T cell surface receptor; cytokine production;
 KW cell proliferation; T cell; infection; autoimmune disease; inflammation;
 KW quality assurance; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT i. .364
 FT /note= "extracellular region"

FT Peptide 1. .20
 FT /note= "signal peptide"
 FT Domain 365. .385
 FT /note= "transmembrane domain"
 FT Domain 386. .432
 FT /note= "cytoplasmic domain"
 XX
 PN W0200008057-A2.
 XX
 PD 17-FEB-2000.
 XX
 XX 05-AUG-1999; 99WO-US017906.
 XX
 XX 07-AUG-1998; 98US-0095663P.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Baum PE;
 XX
 DR WPI; 2000-205674/18.
 DR N-PSDB; AA261416.
 XX
 PT Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 FT costimulatory molecules for therapeutics against infections, autoimmune
 FT diseases and inflammation.
 XX
 PS Claim 8; Page 40-41; 57pp; English.

CC The present sequence represents the long extracellular form of human B7-1
 CC (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine and memory
 CC production, cell proliferation and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the disordered mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting
 CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic
 CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes
 CC which catalyse a colorimetric or fluorometric reaction, may be attached
 CC to a B7L-1 polypeptide, e.g. nitrogen mustards are attached to the B7L-1
 CC and used to treat various forms of cancer

Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 3; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 QY 61 ASQDSQPWTSDETVAAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGKRALDRNRIOIV 120
 Db 61 ASQDSQPWTSDETVAAGTIVLKQVQKHEDSSLOWSNPAQOTLYFGKRALDRNRIOIV 120
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 QY 181 TATLNCQSSGSKPAARLTWRKGDDELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
 Db 181 TATLNCQSSGSKPAARLTWRKGDDELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
 QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPREGQKLLHCEGRGNVPVQOYL 300


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RA Sudhof T.C.;
RT "syncAM, a synaptic adhesion molecule that drives synapse assembly.";
RL Science 0:0-0(2002).
DR EMBL; AF539424; AAN01614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045021; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain.
KW
SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

      Query Match          31.8%;   Score 719.5;   DB 11;   Length 445;
      Best Local Similarity 36.2%;   Pred.No. 4.8e-51;
      Matches 166;   Conservative 75;   Mismatches 140;   Indels 77;   Gaps 1

QY 9 LLLLLFACWAPGGANLSQDGYWQOQDLELGTFLAPLDEAISSTVMSSPDMLASQDSQFW 68
Db 31 LLLLLLSAAALIPTG-----DG---QNL-----F 51

QY 69 TSDPTVAGTVVLKCOVKDHDSSLOWNPAQOITLYFGEKALRDNRLOLVTSTPHELS 12
Db 52 TKDVTVIEGEVATISCOVNKSDSVQLNPNRQTIYFRDFPLKDSRQLLNFSSELK 11

QY 129 ISISNVALADEGEYTCISIFTMPVRTAKSVITVLGIPQKPIITGYKSSIREKDTATLNCQS 18
Db 112 VSLTNVISIDEGRYFCQLYTDPDPQESYTIITVLVPPRNLMIDIKQTAVEGEIEVNCTA 17

QY 189 SGSKPAARLTWRKGDQLHEGPTRIOEDNGKTFTVSSSVTVQVTRDDGASIVCSVNH 24
Db 172 MASKPATTTIRWFNGKNELKKG-SEVEWSD--MYTTSQLMLKVKHKEDGVPVICOQVEHP 22

QY 249 SLKGADRSVSORLEVLYTPTAMIRPDP--HPREGOKLLHCEGKGNPVPQOYLWEK-E 30
Db 229 AVTG-NLQIORYLEVQYKQVHLQMYIPYLOGLTREGDAFELTCEALGKQPMVTWVRVD 28

QY 305 GSVPPKLMTQESALIPFLINKSDGYTCGTATSNMGSYKAYTYTLNVNDPS---PVPSSSS 36
Db 288 DEMFOHVLVSGPNLFINNLKTDNGTYRCEASINVGKASHDSYMLYVYDPTTIPPTTTT 34

QY 362 TY-----HAIIGGIVAFIVFLLLIMLFLGLHYLRHKG 39
Db 348 TTTTWTTSITLTIITDSRAGEGTIGAVDHAVIGGVAVVVFAMLCILLIILGRYFARKG 40

QY 395 TYLTFAKSGDDADPADTAIINAEGQSGGDDKKEYFI 432
Db 408 TYTFEAKGADDAADPADTAIINAEGGNNSEBKEYFI 445

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Search completed: May 27, 2004, 09:34:57
Job time : 36.4266 secs

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001560; BAA91756.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 163 AA; 17860 MW; FB746375A05B0006 CRC64;

Query Match 38.5%; Score 872; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 2.7e-64;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 329
Db 1 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 60

QY 330 TYGCTATSNMGSKAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 389
Db 61 TYGCTATSNMGSKAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 120

QY 390 IRHKGTYLTHEAKGSDPADADTAIINAEQGSGGDDKKEYFI 432
Db 121 IRHKGTYLTHEAKGSDPADADTAIINAEQGSGGDDKKEYFI 163

RESULT 13
Q8KLH8 PRELIMINARY; PRT; 163 AA.
ID Q8KLH8
AC Q8KLH8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to hypothetical protein FLJ10698.
GN NECL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK030782; BAC27137.1; -;
DR MGD; MGI:2137858; Necl1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 163 AA; 17860 MW; FB746375A05B0006 CRC64;

Query Match 34.3%; Score 777; DB 11; Length 152;
Best Local Similarity 96.1%; Pred. No. 1.8e-56;
Matches 146; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 281 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 340
Db 1 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 60

QY 341 SYKAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 400
Db 61 SYTAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 120

QY 401 AKGSDPADADTAIINAEQGSGGDDKKEYFI 432
Db 121 AKGSDPADADTAIINAEQGSGGDDKKEYFI 152

RESULT 15
Q8K3T6 PRELIMINARY; PRT; 445 AA.
ID Q8K3T6
AC Q8K3T6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Body;
RX Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,

Db 61 TYGCTATSNMGSKAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 120
QY 390 IRHKGTYLTHEAKGSDPADADTAIINAEQGSGGDDKKEYFI 432
Db 121 IRHKGTYLTHEAKGSDPADADTAIINAEQGSGGDDKKEYFI 163

RESULT 14
Q8BSQ8 PRELIMINARY; PRT; 152 AA.
ID Q8BSQ8
AC Q8BSQ8
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like 1 (Fragment).
GN NECL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK030782; BAC27137.1; -;
DR MGD; MGI:2137858; Necl1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 152 AA; 16458 MW; E41F6BAAD6A413A7 CRC64;

Query Match 34.3%; Score 777; DB 11; Length 152;
Best Local Similarity 96.1%; Pred. No. 1.8e-56;
Matches 146; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 281 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 340
Db 1 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 60

QY 341 SYKAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 400
Db 61 SYTAYTYLNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 120

QY 401 AKGSDPADADTAIINAEQGSGGDDKKEYFI 432
Db 121 AKGSDPADADTAIINAEQGSGGDDKKEYFI 152

RESULT 15
Q8K3T6 PRELIMINARY; PRT; 445 AA.
ID Q8K3T6
AC Q8K3T6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Body;
RX Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,

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QY 359 SSSTYHAIIGGIVAFIVFLLTLMIFLGHYLRHKGYTLTHEAKGSDPADPADTAINAE 418
DB 322 QNGPDHALIGGIVAVVVFVLTCSIFLLGRYLARKHGYTLTNEAKGAEDPADTAINAE 381
QY 419 GQSGGDDKKKEYFI 432
DB 382 GSQVNAEKKKEYFI 395

RESULT 10
Q8N3J6 PRELIMINARY; PRT; 435 AA.
AC Q8N3J6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DR EMBL; AL834270; CAD36945.1; -.
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein.
GN DKF2P761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amysdaia;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD36945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein, Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 44.9%; Score 1017.5; DB 4; Length 435;
Best Local Similarity 48.6%; Pred. No. 9.6e-76;
Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;

QY 62 SQDSQWTSDETVAGTIVLKCQVXKDESSLOWNSPAQOTLYFGEKALRDNRIQVLT 121
DB 22 SQGQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWSNPAQOTLYFDDKKALRDNRIELVR 81
QY 122 STPHLSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKDT 181
DB 82 ASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSPVMEGL 141
QY 182 ATLNCQSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKTFVSSSVTVQVTRDDGASI 241
DB 142 MQLTCTSGSKPAADIRFWKNDKEIKDVYKLBEDANRKTFTVSSSLDFRVDSDGVAV 201
QY 242 VCSVNHELKAGDRSTQRIEVLVTPMTAMRPPHREGQKLLHCEGRGNVPVQYIWM 301
DB 202 ICRVDHESLNATPQAMQVLEIHYTSPVKLIPTFPQEGQPLITCSKGKLPPEVLW 261
QY 302 EKEGVS---PPLKMTQESALIFFLNKSNGTGTATSNMGSYKAYTILNVND----- 352
DB 382 LCSIPELLGRYLARKHGYTLTNEAKGAEDPADPADTAINAEQSGQVNAEKKKEYFI 435

RESULT 11
Q8I2P8 PRELIMINARY; PRT; 437 AA.
AC Q8I2P8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DR EMBL; AF538973; AAN16368.1; -.
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Nectin-like protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gingrich J.R., D'Angelo A., Chang G.M., Greenberg N.M.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538973; AAN16368.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 44.8%; Score 1014.5; DB 4; Length 437;
Best Local Similarity 48.6%; Pred. No. 1.7e-75;
Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;

QY 62 SQDSQWTSDETVAGTIVLKCQVXKDESSLOWNSPAQOTLYFGEKALRDNRIQVLT 121
DB 24 SQGQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWSNPAQOTLYFDDKKALRDNRIELVR 83
QY 122 STPHLSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKDT 181
DB 84 ASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSPVMEGL 143
QY 182 ATLNCQSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKTFVSSSVTVQVTRDDGASI 241
DB 144 MQLTCTSGSKPAADIRFWKNDKEIKDVYKLBEDANRKTFTVSSSLDFRVDSDGVAV 203
QY 242 VCSVNHELKAGDRSTQRIEVLVTPMTAMRPPHREGQKLLHCEGRGNVPVQYIWM 301
DB 204 ICRVDHESLNATPQAMQVLEIHYTSPVKLIPTFPQEGQPLITCSKGKLPPEVLW 263
QY 302 EKEGVS---PPLKMTQESALIFFLNKSNGTGTATSNMGSYKAYTILNVND----- 352
DB 264 TKDGGELPDPDRMVVSGRELNIPLFKTNGTYRCEATNTIGQSSAEYVLIIVHVDVENTLL 323
QY 353 PSPV-----PSSSSTY-----HAITGGIVAFIVFLL 378
DB 324 PTTIIPSLTATVTTVAITTSPTTSATTSIRDNPALAGQNGPDHALIGGIVAVVVFV 383
QY 379 LIMLIFLGHYLRHKGYTLTHEAKGSDPADPADTAINAEQSGGDDKKKEYFI 432
DB 384 LCSIPELLGRYLARKHGYTLTNEAKGAEDPADPADTAINAEQSGQVNAEKKKEYFI 437

RESULT 12
Q8NVJ5 PRELIMINARY; PRT; 163 AA.
AC Q8NVJ5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DR EMBL; AF538973; AAN16368.1; -.
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Hypothetical protein FLJ10698.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
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Db 204 SDDGVAVICRVDBESLNATPQVAMQVLEIHYTPSVKLIPTSTPPQBGQALTUTCESKGP 263
Qy 295 VPOQYLWEKGSV---PPLKWTQESALIPFLNKS DSGTYGCTATSNMGSYKAYVTLNVN 351
Db 264 LPEPVLWTKGAEPLPDRMVSGRLENIILFLNKTDNGYRCEATNTIGQSSAEYVLIH 323
Qy 352 DPSVPSSSTVHAITGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDAPDAD 411
Db 324 DPNSLAGQNPDHALLIGGIVAVVVFVTLCSIFILGRLARHKGTYLTHEAKGAEADPAD 383
Qy 412 TAILNAEGSGGDDKKEYFI 432
Db 384 TAILNAEGSQVNAEKKKEYFI 404

RESULT 8
Q8BZP4 PRELIMINARY; PRT; 395 AA.
AC Q8BZP4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dienecephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK033973; BAC28533.1; --
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 395 AA; 43516 MW; EB70FB5363D872F3 CRC64;

Query Match 46.0%; Score 1042.5; DB 11; Length 395;
Best Local Similarity 52.9%; Pred. No. 7.1e-78;
Matches 198; Conservative 68; Mismatches 105; Indels 3; Gaps 1;

Qy 62 SQDSQWTSDETAVAGTVVLCQVQKDHEDSSLOWSNPAQOTLYFGKRALRNRIOLVT 121
Db 22 SQGFPLTQNVVVEGTAITLCRVQDNDNTSLQSNPAQOTLYFDDKKALRNRIELVR 81
Qy 122 STPHELSISINVALADEGETCSIFTPMVRTAKSLVTLVIGIPKPIITGYKSSLRKDT 181
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGVPEKPIQSGFSSPVMGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQLHGEPTRIQEDNGKTFVSSSVTFVOTREDDGASI 241
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGVPEKPIQSGFSSPVMGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQLHGEPTRIQEDNGKTFVSSSVTFVOTREDDGASI 241
Db 142 MQLTCKTSGSKPAADIRFKNDEIKDVLYKEDANRKTFTVSTLDFRVDSDGAV 201
Qy 242 VCSVNHSLKGDARSTSRILEVLYTPTAMTRPDPHREGOKLLHCEGRGNVPQOYLW 301
Db 202 ICRVDHESLNATPQVAMQVLEIHYTPSVKLIPTSTPPQBGQALTUTCESKGPBPVLW 261
Qy 302 EKEGSV---PPLKWTQESALIPFLNKS DSGTYGCTATSNMGSYKAYVTLNVNDPSPVPS 358
Db 262 TKDGAELPDRMVSGRLENIILFLNKTDNGYRCEATNTIGQSSAEYVLIHVDPSLAG 321

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Db 262 TKDGAELPDRMVSGRLENIILFLNKTDNGYRCEATNTIGQSSAEYVLIHVDPSLAG 321
Qy 359 SSTVHAITGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDAPDADTAIINAE 418
Db 322 QNGPHALIGGIVAVVVFVTLCSIFILGRLARHKGTYLTHEAKGAEADPADTAIINAE 381
Qy 419 GQSGGDDKKEYFI 432
Db 382 GQVNAEKKKEYFI 395

RESULT 9
Q8BXJ7 PRELIMINARY; PRT; 395 AA.
AC Q8BXJ7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK046800; BAC32876.1; --
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; IG; 3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 395 AA; 43517 MW; E57E1BBD6D3672F9 CRC64;

Query Match 46.0%; Score 1042.5; DB 11; Length 395;
Best Local Similarity 52.9%; Pred. No. 7.1e-78;
Matches 198; Conservative 68; Mismatches 105; Indels 3; Gaps 1;

Qy 62 SQDSQWTSDETAVAGTVVLCQVQKDHEDSSLOWSNPAQOTLYFGKRALRNRIOLVT 121
Db 22 SQGFPLTQNVVVEGTAITLCRVQDNDNTSLQSNPAQOTLYFDDKKALRNRIELVR 81
Qy 122 STPHELSISINVALADEGETCSIFTPMVRTAKSLVTLVIGIPKPIITGYKSSLRKDT 181
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGVPEKPIQSGFSSPVMGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQLHGEPTRIQEDNGKTFVSSSVTFVOTREDDGASI 241
Db 142 MQLTCKTSGSKPAADIRFKNDEIKDVLYKEDANRKTFTVSTLDFRVDSDGAV 201
Qy 242 VCSVNHSLKGDARSTSRILEVLYTPTAMTRPDPHREGOKLLHCEGRGNVPQOYLW 301
Db 202 ICRVDHESLNATPQVAMQVLEIHYTPSVKLIPTSTPPQBGQALTUTCESKGPBPVLW 261
Qy 302 EKEGSV---PPLKWTQESALIPFLNKS DSGTYGCTATSNMGSYKAYVTLNVNDPSPVPS 358
Db 262 TKDGAELPDRMVSGRLENIILFLNKTDNGYRCEATNTIGQSSAEYVLIHVDPSLAG 321

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QY 1 MGAPAAALLLLLLLACCWAPGANLSQDQWQOEQLGTLAPLDEALISSTVWSPDML 60
Db 1 MGAPASALLLLLLLACCWAPGANLSQD-----29
QY 61 ASOSQPWTSDETVVAGTGVVVKQVKDHEDSSLOWNSNPAQOTLYFGKALRDNRIQLV 120
Db 30 --DSQPWTSDETVVAGTGVVVKQVKDHEDSSLOWNSNPAQOTLYFGKALRDNRIQLV 86
QY 121 TSTPHELISISINVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSUREKD 180
Db 87 TSTPHELISISINVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSUREKD 146
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVTVSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPND-----185
QY 241 IVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHPREGOKLLHCEGRGNPVPQOYL 300
Db 186 -----TPTAMIRDPDPHPREGOKLLHCEGRGNPVPQOYL 220
QY 301 WEKEGSVPPLKMTQ 314
Db 221 WEKEGSVPPLKMTQ 234
RESULT 6
Q8BYP1 PRELIMINARY; PRT; 404 AA.
AC Q8BYP1
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK038842; BAC30148.1; -;
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44387 MW; E9C84191AA687473 CRC64;
Query Match 46.1%; Score 1043.5; DB 11; Length 404;
Best Local Similarity 52.2%; Pred. No. 6.1e-78;
Matches 199; Conservative 69; Mismatches 110; Indels 3; Gaps 1;
QY 55 SSPDMLASQSQPWTSDETVVAGTGVVVKQVKDHEDSSLOWNSNPAQOTLYFGKALRDN 114
Db 24 SKSVKVGSGQGFPLTONVTVVGGTALTCTCRVDQNDNTSLQWSNPAQOTLYFDDKKALRD 83
QY 115 NRILQVTSSTPHELISISINVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 174
Db 84 NRILVRSWHELISISVDSLSDEGQYTCISFTMPVKTSKAYLTVLGVPEKQIQISGFS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVTVSSVTFQVTR 234
Db 84 NRILVRSWHELISISVDSLSDEGQYTCISFTMPVKTSKAYLTVLGVPEKQIQISGFS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVTVSSVTFQVTR 234
Db 144 PVMEGDLMLQTLTKTSGSKPAADIRWFNFNDKEIKDVYKLEEDANRKTFTVSSITLDFRVD 203
QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHPREGOKLLHCEGRGNP 294
Db 144 PVMEGDLMLQTLTKTSGSKPAADIRWFNFNDKEIKDVYKLEEDANRKTFTVSSITLDFRVD 203
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QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHPREGOKLLHCEGRGNP 294
Db 204 SDGVAVICRVHESLNATPQVAMQVLEIHTPSVKLIIFSTFPQEQALTLTCSKGRP 263
QY 295 VPQYLWEKEGSV--PPLKMTQESALIFPFLNKSDSGTCTATSNMGSYKAYTYTLNVN 351
Db 264 LPEPVLTKDGAELPDPDRMVVSGRELNFLENKTDNGTYRCCKATNTIQSSSAEYVLIVH 323
QY 352 DSPSPVSSSTYHAIIGGIVAFIVFLLLMFLHGLYLRHKGYTLTHEAKGSDDDPAD 411
Db 324 DPNSLAQGNPDPHALGGIVAVVVFVTLCSIFLLGRTARHKGYTLTNKAKGAEDPAD 383
QY 412 TAINAEGSGSGDDKKEYFI 432
Db 384 TAINAEGSQVNAEKEKEYFI 404
RESULT 7
Q8BLQ9 PRELIMINARY; PRT; 404 AA.
AC Q8BLQ9
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK043760; BAC31646.1; -;
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; Ig; 3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44388 MW; 091E493B82CAF5B CRC64;
Query Match 46.1%; Score 1043.5; DB 11; Length 404;
Best Local Similarity 52.2%; Pred. No. 6.1e-78;
Matches 199; Conservative 69; Mismatches 110; Indels 3; Gaps 1;
QY 55 SSPDMLASQSQPWTSDETVVAGTGVVVKQVKDHEDSSLOWNSNPAQOTLYFGKALRDN 114
Db 24 SKSVKVGSGQGFPLTONVTVVGGTALTCTCRVDQNDNTSLQWSNPAQOTLYFDDKKALRD 83
QY 115 NRILQVTSSTPHELISISINVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 174
Db 84 NRILVRSWHELISISVDSLSDEGQYTCISFTMPVKTSKAYLTVLGVPEKQIQISGFS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVTVSSVTFQVTR 234
Db 144 PVMEGDLMLQTLTKTSGSKPAADIRWFNFNDKEIKDVYKLEEDANRKTFTVSSITLDFRVD 203
QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHPREGOKLLHCEGRGNP 294
Db 144 PVMEGDLMLQTLTKTSGSKPAADIRWFNFNDKEIKDVYKLEEDANRKTFTVSSITLDFRVD 203
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RT 60.770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF195662; AAG35584.1; -
DR EMBL; AY059393; AAL29691.1; -
DR EMBL; AK038917; BAC30168.1; -
DR EMBL; AK053077; BAC35258.1; -
DR MGD; MGI:2137858; Nccl1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; CIADF8B57D141F3A CRC64;

Query Match 85.8%; Score 1943; DB 11; Length 396;
Best Local Similarity 87.3%; Pred. No. 1.8e-152;
Matches 377; Conservative 11; Mismatches 8; Indels 36; Gaps 2;

QY 1 MGAPASLILLLLFACWAPGANLSQDGYWQEQDLEGLTAPLDEALISVTWSSPDML 60
DB 1 MGAPSA--LPLLLLLACSWAPGANLSQD----- 27

QY 61 ASQDSQPWTSDETVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQ 120
DB 28 ---DSQPWTSDETVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQ 84

QY 121 TSTPHELISISNVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKD 180
DB 85 SSTPHELISISNVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKE 144

QY 181 TATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSVTFQVTRDDGAS 240
DB 145 TATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSVTFQVTRDDGAS 204

QY 241 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQYL 300
DB 205 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQV 264

QY 301 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSS 360
DB 265 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSS 324

QY 361 STYHAIIGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDADPADTAINAEGG 420
DB 325 STYHAIIGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDADPADTAINAEGG 384

QY 421 QSGGDDKKEYFI 432
DB 385 QSGGDDKKEYFI 396

RESULT 4
Q7ZXX1 PRELIMINARY; PRT; 394 AA.
AC Q7ZXX1;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to nectin-like 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044084; AAH44084.1; -

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS0835; IG LIKE; 3.
SQ SEQUENCE 394 AA; 42730 MW; F1141D8E6B69254A CRC64;

Query Match 55.8%; Score 1262.5; DB 13; Length 394;
Best Local Similarity 64.8%; Pred. No. 4.2e-96;
Matches 239; Conservative 51; Mismatches 78; Indels 1; Gaps 1;

QY 65 SQPWTSDTVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQVHTSP 124
DB 26 SQPVTADVIVTGGTATLTKCTVQEHLESSLQSNTPAQOTLYFGKRALRDNRILQVHSP 85

QY 125 HELSISINVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKDTATL 184
DB 86 NELTISINVVLSDEGEYTCISFTMPVTRTAKAVVTVLGVPOKQVSGFSAFKENDKAKL 145

QY 185 NCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSVTFQVTRDDGASIVCS 244
DB 146 RCTTSGSGKPAANIKWYKGPPELEGAKTSLVDGNGKTFVKSFIETVTRKDDGAEITCA 205

QY 245 VNHSLSKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQYLWEKE 304
DB 206 VGHSLHDSAKSSSHKIQVQYKPTAKIESRPSMPREGDKLALQCDAYGNVPVDPNVWERE 265

QY 305 -GSVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSYKAYITLVNDPSPVPSSSTY 363
DB 266 NGEVELLANIEGNSLVFENLNKTDGTYTCASNTLGTFTHYKLDVNDPSPIPSTSID 325

QY 364 HAITGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDADPADTAINAEGGQSG 423
DB 326 HAVIGGVAVATFLFCLLIIVLGRYLIHKGTYLTAEAGSDDADPADTAINAEGGQSG 385

QY 424 GDDKKEYFI 432
DB 386 SDDKKEYFI 394

RESULT 5
Q8IZQ9 PRELIMINARY; PRT; 234 AA.
AC Q8IZQ9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Dendritic cell nectin-like protein 1 short isoform (Fragment).
GN NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keryanov S.A., Gardner K.L.;
RT "Alternatively splicing forms of the human nectin V gene.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529206; AAN75603.1; -
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 3.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 25655 MW; 8DA496486BE1CCB CRC64;

Query Match 51.9%; Score 1176; DB 4; Length 234;
Best Local Similarity 74.2%; Pred. No. 2.9e-89;
Matches 233; Conservative 0; Mismatches 1; Indels 80; Gaps 2;

```

Db 1 MGAPASALLLLLLFACCCWAPGAGNLSQDGYWQDLELGTALPLDEAISSTVWSSPDML 60
QY 61 ASQDSQWTSDETVVAGTTLVKQVQKHEDSSLOWSNPAQOITLYFGEKALDRNRILQV 120
Db 61 ASQDSQWTSDETVVAGTTLVKQVQKHEDSSLOWSNPAQOITLYFGEKALDRNRILQV 120
QY 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPPPHREGQKLLHCEGRGNVPVPOYL 300
Db 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPPPHREGQKLLHCEGRGNVPVPOYL 300
QY 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNNDPSPVSSS 360
Db 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNNDPSPVSSS 360
QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLRHKGYTLTHEAKGSDADPADTALINAE 420
Db 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLRHKGYTLTHEAKGSDADPADTALINAE 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 2

Q8N126 PRELIMINARY; PRT; 398 AA.
ID Q8N126
AC Q8N126
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain immunoglobulin receptor precursor (Nectin-like protein 1)
DE (TSLC1-like 1).
GN TSLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Cunningham S.A., Tran T.M., Arrate M.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
[2]
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
[3]
RC TISSUE=Brain;
RA Fukuhara H., Murakami Y.;
RL "Isolation of the TSLC1 and TSLC2 genes, members of the tumor suppressor TSLC1 gene family encoding transmembrane proteins.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY046418; AAL02143.1; -;
DR EMBL; BC033819; AAL033819.1; -;
DR EMBL; AF363367; AAM60749.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.

KW Immunoglobulin domain; Receptor; Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 398 AA; 43300 MW; 601B2FB5D512DB6C CRC64;
Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 4.4e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPASALLLLLLFACCCWAPGAGNLSQDGYWQDLELGTALPLDEAISSTVWSSPDML 60
Db 1 MGAPASALLLLLLFACCCWAPGAGNLSQD----- 29
QY 61 ASQDSQWTSDETVVAGTTLVKQVQKHEDSSLOWSNPAQOITLYFGEKALDRNRILQV 120
Db 30 --DSQWTSDETVVAGTTLVKQVQKHEDSSLOWSNPAQOITLYFGEKALDRNRILQV 86
QY 121 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELSISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPPPHREGQKLLHCEGRGNVPVPOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPPPHREGQKLLHCEGRGNVPVPOYL 266
QY 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNNDPSPVSSS 360
Db 267 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVNNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLRHKGYTLTHEAKGSDADPADTALINAE 420
Db 327 STYHAIIGGIVAFIVFLLLMILIFLGHYLRHKGYTLTHEAKGSDADPADTALINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 3

Q99N28 PRELIMINARY; PRT; 396 AA.
ID Q99N28
AC Q99N28;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein) (Nectin-like 1).
GN NECL1 OR TSLC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RL "Cloning and expression analysis of novel mouse cDNA encoding a membrane protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
[2]
RC SEQUENCE FROM N.A.
RA Fukami T., Maruyama T., Murakami Y.;
RL "Identification of a murine ortholog of the TSLC1-like gene 1.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[3]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Head, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 35.4266 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPASLILLLLLLAFACWA.....AIIAEGGQSGGDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	432	4 Q9UJ1	Q9UJ1 homo sapien
2	2059	90.9	398	4 Q8N126	Q8N126 homo sapien
3	1943	85.8	396	11 Q9N28	Q9N28 mus musculus
4	1762.5	55.8	394	13 Q7XX1	Q7XX1 xenopus lae
5	1176	51.9	234	4 Q81Q9	Q81Q9 homo sapien
6	1043.5	46.1	404	11 Q8BY1	Q8BY1 mus musculus
7	1043.5	46.1	404	11 Q8BLQ9	Q8BLQ9 mus musculus
8	1042.5	46.0	395	11 Q8BZP4	Q8BZP4 mus musculus
9	1042.5	46.0	395	11 Q8BXJ7	Q8BXJ7 mus musculus
10	1017.5	44.9	435	4 Q8N3J6	Q8N3J6 homo sapien
11	1014.5	44.8	437	4 Q812P8	Q812P8 homo sapien
12	872	38.5	163	4 Q9NVJ5	Q9NVJ5 homo sapien
13	831	36.7	163	11 Q8K1H8	Q8K1H8 mus musculus
14	777	34.3	152	11 Q8BSQ8	Q8BSQ8 mus musculus
15	719.5	31.8	445	11 Q8K3T6	Q8K3T6 mus musculus
16	719.5	31.8	445	11 Q8R4L1	Q8R4L1 mus musculus

17	719	31.8	442	4 Q9BY67	Q9BY67 homo sapien
18	710.5	31.4	417	11 Q7TNL1	Q7TNL1 mus musculus
19	709	31.3	456	11 Q8R5M8	Q8R5M8 mus musculus
20	707.5	31.2	443	4 Q8N2F4	Q8N2F4 homo sapien
21	594	26.2	388	4 Q8NFZ8	Q8NFZ8 homo sapien
22	583	25.8	388	11 Q8R464	Q8R464 mus musculus
23	576.5	25.5	381	4 Q9Y4A4	Q9Y4A4 homo sapien
24	514	22.7	295	11 Q9QYL6	Q9QYL6 mus musculus
25	510	22.5	295	11 Q9Z2H8	Q9Z2H8 mus musculus
26	508.5	22.5	306	11 Q9QYL4	Q9QYL4 mus musculus
27	503.5	22.2	278	11 Q9QYL3	Q9QYL3 mus musculus
28	499	22.0	289	11 Q9QYL5	Q9QYL5 mus musculus
29	457	20.2	333	4 Q8GWB8	Q8GWB8 homo sapien
30	454.5	20.1	336	11 Q9D6E7	Q9D6E7 mus musculus
31	454.5	20.1	336	11 Q8OVG4	Q8OVG4 mus musculus
32	328.5	14.5	403	6 Q8HY15	Q8HY15 lemur catta
33	295	13.0	412	6 Q8HY14	Q8HY14 cryptolagus
34	273.5	12.1	401	6 Q88835	Q88835 cercopithec
35	272	12.0	778	4 Q81ZU9	Q81ZU9 homo sapien
36	271	12.0	779	4 Q96JG0	Q96JG0 homo sapien
37	271	12.0	612	11 Q8BGQ5	Q8BGQ5 mus musculus
38	271	12.0	766	11 Q81OH3	Q81OH3 mus musculus
39	271	12.0	778	11 Q8BR86	Q8BR86 mus musculus
40	264	11.7	417	4 Q96B5J1	Q96B5J1 homo sapien
41	264	11.7	439	13 Q57349	Q57349 gallus gall
42	256	11.3	530	11 Q80XJ5	Q80XJ5 mus musculus
43	255	11.3	412	11 Q63611	Q63611 rattus norv
44	255	11.3	412	11 Q9R1E1	Q9R1E1 rattus norv
45	254.5	11.2	467	11 Q91VT9	Q91VT9 mus musculus

ALIGNMENTS

RESULT 1
Q9UJ1 PRELIMINARY; PRT; 432 AA.
ID Q9UJ1
AC Q9UJ1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BK134P22.1 (Novel protein similar to mouse IMMUNOSUPERFAMILY protein BL2) (NECTIN-like protein 1).
GN BK134P22.1 OR NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Yuan J., Qiang B.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035403; CAB56227.1; -.
DR EMBL; AF062733; AAD17540.2; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 432 AA; 47020 MW; AC474EFEC4C518C CRC64;

Query Match 100.0%; Score 2264; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 5, 2e-179;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLILLLLLLAFACWA.....AIIAEGGQSGGDKKEYFI 432

DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; Ig; 5.
DR PRINTS; PR01472; ICAMVCAM1.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 5.
KW Immunoglobulin domain; Glycoprotein; Cell adhesion; Transmembrane;
Repeat; Signal.
FT SIGNAL 1 24 PROBABLE.
FT CHAIN 25 739 VASCULAR CELL ADHESION PROTEIN 1.
FT DOMAIN 25 698 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 699 720 POTENTIAL.
FT DOMAIN 721 739 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 111 IG-LIKE C2-TYPE 1.
FT DOMAIN 119 212 IG-LIKE C2-TYPE 2.
FT DOMAIN 223 309 IG-LIKE C2-TYPE 3.
FT DOMAIN 312 397 IG-LIKE C2-TYPE 4.
FT DOMAIN 408 506 IG-LIKE C2-TYPE 5.
FT DOMAIN 514 595 IG-LIKE C2-TYPE 6.
FT DOMAIN 601 682 IG-LIKE C2-TYPE 7.
FT DISULFID 47 95 BY SIMILARITY.
FT DISULFID 52 99 BY SIMILARITY.
FT DISULFID 137 195 BY SIMILARITY.
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 739 AA; 81246 MW; 5C608E5A1A1B100C CRC64;

Query Match 9.5%; Score 215; DB 1; Length 739;
Best Local Similarity 26.4%; Pred. No. 1.1e-07;
Matches 112; Conservative 45; Mismatches 176; Indels 92; Gaps 23;

QY 66 QPWTSD---ETVVA--GGTVVLKQVKDHSDSLOWNPAAQQTLYFGEKRALRDNRIQL 119
Db 311 KPFTVDISQSQVAAQVGSVLTCAAVGCDSPFSFWRQTDSPLN-GE---VRD---EG 363
QY 120 VTSSTPHELISISNVALADEGYTCISFTWMPRTAKSL-VTVLIGIPKPIITGYKSSLRE 178
Db 364 ATST----LTLSPVGVEDSHSLCTVTCORRLEKTIQVEVYVFFEDPEIE-ISGPLVH 417
QY 179 KDTATLNCQSSGSKPAARLTWRKQDQLHGEPTP-----TOEDPNGKTF-TVSSSVTFQVT 233
Db 418 GREVTVNCVTPVNYPPFDHLE-----IELKGETTLNKLFLREEIGTKSLETKSLEMTFPT 473
QY 234 REDDGASIVGSVN-HESLKGADRSTQSRIEVLVT-----PTAMIRPDPPHREGQKLL 286
Db 474 AEDTGKALVCLAKHSQSEPKQKQSTQTLVNVNAPKEPTIWSVSPV-PREGSPVNL 532
QY 287 HCEGRNPVPQQYLWE---KEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYK 343
Db 533 TCSSDGFPTP-KILWSKQLKNGELQPL--SQNTLSFMATKMEDSGIYVCEGINEAGISK 589
QY 344 AYTLANVDPS-----PVPSSSTYHAIIG--GIYAFIVFLJ-----LIMLIF 384
Db 590 KVELIIQSSKDIQLTVFPKSKVEGDTVIIISCTGSPVEPIWILKKAKTGDWIKSV 649
QY 385 LGHYLIR-----HKGTY-----LTHEAKGSDADP-----ADTAI 414
Db 650 NGSYTIKKAQLQDAGVYECSEKTEVGSQLSRLTLDYKGNKNDYFSPPELLALYFASLV 709
QY 415 INAEG 419
Db 710 IPAIG 714


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CC or send an email to license@sib-ch).
CC -----
CC EMBL; U95030; AAC06342.1; -.
CC DR EMBL; L25274; AAA37528.1; -.
CC DR HSSP; Q13740; 1KJC.
CC DR MGD; MGI:1313266; Alcam.
CC DR GO; GO:0019997; C:extrinsic to plasma membrane; IDA.
CC DR GO; GO:0007165; P:signal transduction; IPI.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig; 4.
CC DR SMART; SM00409; Ig; 3.
CC DR PROSITE; PS00835; IG-LIKE; 4.
CC DR PROSITE; PS00290; IG_MHC; FALSE NEG.
CC KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 120 IG-LIKE V-TYPE 1.
FT DOMAIN 125 234 IG-LIKE V-TYPE 2.
FT DOMAIN 245 328 IG-LIKE C2-TYPE 1.
FT DOMAIN 333 409 IG-LIKE C2-TYPE 2.
FT DOMAIN 416 501 IG-LIKE C2-TYPE 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 227 232 PSEGKT -> AAGIPA (IN REF. 2).
FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SEQUENCE 583 AA; 65161 MW; E7BAFA8FCABF9489 CRC64;

Query Match 9.6%; Score 217.5; DB 1; Length 583;
Best Local Similarity 24.1%; Pred. No. 5.3e-08;
Matches 89; Conservative 49; Mismatches 143; Indels 89; Gaps 15;

QY 77 GGTVLKQVCKDHEDSLQNSPAQOTLYRGEK-----ALRDNRIQLV----- 120
Db 36 GDTIVMPCRL-----DVPQNLMFGRKWKYKPDGSPVFIARSTKKSQVDDV 83

QY 121 -----TSTPHELSISISVALADEGYTCISFMP-VRTAKSLVTVLGIPOKPIITGYK 173
Db 84 PEYKDRLSLSENYTLISANAKISDEKFCVCLVTEDEVFEAPLVKFKQSPKEIVNKA 143

QY 174 SSIREKDTATL-NCQSGSGSPARLTW-RKGD--QELHGEP-----RIQEDPNKGTFTVSS 226
Db 144 PFLETDLQKLGLGICISDSYDPDGNITWYRNGKVLQPVGEVAILFKKEIDPGTQLYTVTS 203

QY 227 SVTFQVTRDDGASIVCSNVHESLKGADRTS-ORIEVLYTPTAMIR-----PDPHPREG 281
Db 204 SLEKTRTRSDIQMPTFCVTVYSGSGKTYISEQEIFDIYPTQVTVLPPKNAIKEG 263

QY 282 QKLLHCEGRGNVPVQOYLMEKEGSPFLKMTQESALIFPFLANKSDSGTCTATS--NM 339
Db 264 DNITLQCLGNGNPPPEFMYFLPQ--PEGIRSNSTYTLTDVRENATGDKCSLIDKKNM 321

QY 340 GSKA-----YTLNVN-----DPSV-----PSSSS 361
Db 322 AASTITVHYLDLSINPRGEVTKIGDTLPVSCITISASRNATVMMKDNIRLSRSPSS 381
QY 362 TYHAIGGIV 371
```

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Db 382 LHYQDAGNYV 391
:: | |
RESULT 14
ID CEAS_HUMAN STANDARD; PRT; 702 AA.
AC P06731;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 5 precursor
DE (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e
DE antigen).
GN CEACAM5 OR CEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90258861; PubMed=2342461;
RA Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
RA Hassauer M., Shively J.E., von Kleist S., Zimmermann W.,
RT "Cloning of the complete gene for carcinoembryonic antigen: analysis
RT of its promoter indicates a region conveying cell type-specific
RT expression.";
RT Mol. Cell. Biol. 10:2738-2748(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038876; PubMed=3670312;
RA Beauchemin N., Benchimol S., Cournoyer D., Fuks A., Stanners C.P.;
RT "Isolation and characterization of full-length functional cDNA clones
RT for human carcinoembryonic antigen.";
RX Mol. Cell. Biol. 7:3221-3230(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89122014; PubMed=3220478;
RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT "Carcinoembryonic antigen family: characterization of cDNAs coding
RT for NCA and CEA and suggestion of nonrandom sequence variation in
RT their conserved loop-domains.";
RX Genomics 3:59-66(1988).
RN [4]
RP SEQUENCE OF 5-702 FROM N.A.
RX MEDLINE=87128144; PubMed=3814146;
RA Oikawa S., Nakazato H., Kosaki G.;
RT "Primary structure of human carcinoembryonic antigen (CEA) deduced
RT from cDNA sequence.";
RX Biochem. Biophys. Res. Commun. 142:511-518(1987).
RN [5]
RP SEQUENCE OF 331-702 FROM N.A.
RX MEDLINE=87204247; PubMed=3033671;
RA Zimmermann W., Ortlieb B., Friedrich R., von Kleist S.;
RT "Isolation and characterization of cDNA clones encoding the human
RT carcinoembryonic antigen reveal a highly conserved repeating
RT structure.";
RX Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Found in adenocarcinomas of endoderally
CC derived digestive system epithelium and fetal colon.
CC -1- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 kDa
CC COMPRISING 60% CARBOHYDRATE.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like domains.
CC -1- DATABASE: NAME=CEA; NOTE=CD guide CD66e entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd66e.htm".
CC -----
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DR PROSITE; PS00290; IG MHC; FALSE NEG.
KW Repeat; Signal; Transmembrane; Immunoglobulin domain; SH3-binding;
KW Glycoprotein; Phosphorylation; Polymorphism.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 506 PROTEIN-TYROSINE PHOSPHATASE NON-RECEPTOR
FT TYPE SUBSTRATE 1.
FT DOMAIN 30 371 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 372 392 POTENTIAL.
FT DOMAIN 393 506 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 145 IG-LIKE V-TYPE.
FT DOMAIN 148 248 IG-LIKE C1-TYPE 1.
FT DOMAIN 255 348 IG-LIKE C1-TYPE 2.
FT DISULFID 55 121 POTENTIAL.
FT DISULFID 170 228 POTENTIAL.
FT DISULFID 273 331 POTENTIAL.
FT SITE 432 435 SH2-BINDING (POTENTIAL).
FT SITE 441 446 SH3-BINDING (POTENTIAL).
FT SITE 455 458 SH2-BINDING (POTENTIAL).
FT SITE 472 475 SH2-BINDING (POTENTIAL).
FT SITE 498 501 SH2-BINDING (POTENTIAL).
FT MOD_RES 431 431 PHOSPHORYLATION (BY TYR-KINASES) (POTENTIAL).
FT MOD_RES 455 455 PHOSPHORYLATION (BY TYR-KINASES) (POTENTIAL).
FT MOD_RES 472 472 PHOSPHORYLATION (BY TYR-KINASES) (BY SIMILARITY).
FT MOD_RES 498 498 PHOSPHORYLATION (BY TYR-KINASES) (BY SIMILARITY).
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 179 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 23 23 T -> S.
FT VARIANT 28 28 T -> A.
FT VARIANT 61 61 S -> L.
FT VARIANT 70 70 K -> R.
FT VARIANT 120 120 Y -> H.
FT VARIANT 125 125 R -> Q.
FT VARIANT 127 127 E -> G.
FT VARIANT 129 129 R -> V.
FT VARIANT 132 132 M -> H.
FT VARIANT 145 145 S -> N.
FT VARIANT 153 153 L -> V.
FT VARIANT 203 203 N -> D.
FT VARIANT 261 261 G -> R.
FT VARIANT 302 302 F -> L.
FT VARIANT 316 316 F -> L.
FT VARIANT 337 337 G -> R.
FT VARIANT 367 367 S -> N.
FT VARIANT 422 422 Q -> L.
FT VARIANT 429 429 I -> F.
FT VARIANT 433 433 D -> E.
SQ SEQUENCE 506 AA; 55093 MW; 6B7E310677FCF9CB CRC64;
Query Match 9.6%; Score 217.5; DB 1; Length 506;
Best Local Similarity 22.3%; Pred. No. 4.4e-08;
Matches 102; Conservative 71; Mismatches 178; Indels 107; Gaps 21;
QY 8 LLLLLLACWAPGGANLSQDGYWQBDLELGTAPLDEAISTVWSSPDMLASQDSQP 67
Db 14 LLLCILLAAASNAWT-GTAG-----DGEIQVIQP-ERSVS----- 44
QY 68 WTSDETIVAGTGVVLCQVKDHD-SSLOW---SNPAQQTLYGKEKALDRNRIQLVTST 123

Db 45 -----VAAGETATLHCTVTSLSVPGPIKWFKGTGPGREFIY-SQKEAPFPRTVNVSDAT 97
QY 124 PH--ELSTISNVALADBEVTCISFTMPRTAKSL-----VTVLGIPQKPIITGYK 173
Db 93 KKNMDFSIIRISNITPADAGVYCVKFRKEKGMDFKSGPGTHLTVSAKPPVLSGPT 157
QY 174 SSLREKDTATLNCQSSGSKPA-ARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQV 232
Db 158 VRATPEQTWNFTCTSHGFSRNLKWKFKNGNELSASQTSVDPEDNNVSYSINSTEKVL 217
QY 233 TREDGASIVSNHESLKAD--RSTSORIEVLTPAMIRPDPPHREGOKLLHCR- 289
Db 218 ATGDVHSQVCEVAHVTLQGGPPLRGATNLSTIRVPPTL--EITGSPAGNQVNVTCQV 275
QY 290 GRGNVPVPOQYLWEKEGSPVPLKMTQESALIPFLNKSQSGTYGCTATSNMGS----- 341
Db 276 NKFYRHLQLTWLENGM-----SRTEAASVTV---ENKDGTFNQISWFLVNSAAREAV 328
QY 342 -----YKAYTYLNVNDP-----SPVSSS--STYHAIIGGIVAFIVFLL 379
Db 329 LTCQVEHDQPAVSKNHTLEVSAPQKQDTGTPGPNDSNMTSIFIVGVWCALLVALLI 388
QY 380 IMLIFLGHVLIHKGTYLTHEAKGSDA-----PDADT 412
Db 389 AAL-----YLLRIR---QNKAKGSTSTRLHEPEKNT 417
RESULT 13
C166_MOUSE STANDARD; PRT; 583 AA.
ID C166_MOUSE 070136;
AC Q61490; O70136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM) (DM-GRASP protein).
DE ALCAM.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D., Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is conserved in different homologs and mediates cross-species binding."; Eur. J. Immunol. 27:1469-1478(1997).
RN [2]
RP SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.F.;
RT "The molecular cloning and characterization of potential chick DM-GRASP homologs in zebrafish and mouse."; J. Neurobiol. 25:831-845(1994).
CC -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC EMBL; Y081171; CAA69357.1; -.
CC EMBL; Z94720; CAB08115.1; -.
DR DR EMBL; Z94720; CAB08115.1; Ig-like.
DR InterPro; IPR007110; Ig-Like.
DR DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
KW Membrane; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 315 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT FT PROTEIN.
FT PROPPEP 316 338 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 29 122 IG-LIKE C2-TYPE 1.
FT DOMAIN 132 214 IG-LIKE C2-TYPE 2.
FT DOMAIN 219 306 IG-LIKE C2-TYPE 3.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 153 197 POTENTIAL.
FT DISULFID 239 290 POTENTIAL.
FT LIPID 315 315 GPI-anchor amidated asparagine
(POTENTIAL).
FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 338 AA; 37394 MW; 8FA4A60AD98426B4 CRC64;

Query Match 9.9%; Score 225; DB 1; Length 338;
Best Local Similarity 27.4%; Pred. No. 7.3e-09;
Matches 79; Conservative 42; Mismatches 137; Indels 30; Gaps 13;

QY 62 SQDSQPWTSDETIVAGTGVVVKQVDHEDSSQLQWSNPAQTLLYFGKRALRDNRKIOLVT 121
Db 31 SVDPTFRGTDNITVRQGDTAILRCRFVED-RSSKVAWLN-RSGIIFAGEDKNSLDPRVELEK 88

QY 122 STPHESISISNVALADEGYTCISFTMPVRTAKSLTVILGIPOKPIITGYKSSLREKDT 181
Db 89 RSPLEYSLSLRQKVDVDEGSYTCSVQGHHPKTSQVYLIVQVPFKISNISSDITVNEGSN 148

QY 182 ATLNCOSSGSKPAARLTWRKGDOELHGCEPTRIOBDPNKGKFTVSSSV--TFQVTRDDGA 239
Db 149 VTLVCWANG-RPEPVITWR-----HLTPT-----GKEFEGEVEYLEILGITREQSG- 193

QY 240 SIYCVSNHESLKADRSSTORIEVLVYPTMTAMIRDPDPHPREGQKLHLHCGRGNPVPQQY 299
Db 194 KYECKAANE-VASAD-VKQVRVTWNVPPT-ITESKSNEAATGROALLRCEASAVPTP-DF 249

QY 300 LWKEK-----GSVPPLKMT-QESALFFPFINKSDSYGTGTAASNMG 340
Db 250 EWYRDDTRINSANGLEIKSTGSSLLMVANVTBEHYGNYTCVAANKLG 297

RESULT 11
KILO_RAT ID KATO RAT STANDARD; PRT; 348 AA.
AC Q9Z0J8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE DE Kilon protein precursor (Kindred of IgION).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
MEDLINE=99175207; PubMed=10075727;

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Query Match 10.0%; Score 225.5; DB 1; Length 538;
Best Local Similarity 23.9%; Pred. No. 1.3e-08;


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FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 L -> P (IN REF. 1).
FT CONFLICT 136 136 N -> D (IN REF. 1).
FT CONFLICT 165 165 P -> PP (IN REF. 2).
FT CONFLICT 342 342 S -> G (IN REF. 3).
FT CONFLICT 428 428
SQ SEQUENCE 515 AA; 57064 MW; PFF608EB5F7A0F CRC64;

Query Match
Best Local Similarity 10.1%; Score 228.5; DB 1; Length 515;
Matches 112; Conservative 59; Mismatches 153; Indels 103; Gaps 26;

QY 77 GGTVLKQVCKDHDS---SLQW---SNPAQQLTYFGEKRALDRNIQLVTSPPHEL-- 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKASNGSKQW-----AIPTMGVSVLPPIEKRV 97
QY 128 -----SISISNVALADEGEYTCSTFTMPVTRAKSLVTLGIPQKPI--ITGYKSS 175
Db 98 EFLRPSFDIGTIRLSGLELEDEGMVYICFATFTPTGNRESQLN-LTVMAKPTNWIEGTRAV 156
QY 176 LREK---DTATL--NCQSSGSKPARLITWRKGDQELHGEPTRIQ--DPNGKFTFVSSSV 228
Db 157 LRARKGDQNVKLVATCTSAANGKPSAVSW---ETRLKGE-AEYQEIKNPG-TVTVISRY 211
QY 229 TFQVTRDDGASIVCSVNVHESLKGADR-STSORTEVLYTPTAMIRP-DPPHREGQKILL 286
Db 212 RLVPSEARHQSLACIVNYH---LDPRFSLTNVOYEVEVTEIGEDGNWYLORTDVKL 267
QY 287 HCEGRGNVPQOYLWEK-EGSVPLPKMTQESALIP--PFLNKSDSGTYGCTATSNMGYSX 343
Db 268 TKRADANPPATEYHWITLNGSLPKGVAQNRTLPFRGP-ITYSLAGTYICEATNPICTRS 326
QY 344 AYTLLVND-----PSP-----VPSSSTYHAIIGGIVAFIVFLILLMIFLGHYLI- 390
Db 327 GOVEVNITFPPTPTPHGRAGOMPT-----AIIQGVAGSV-----LLVLIVVGGIIVA 376
QY 391 ----RH--KGYLT-----HEAGSDDPADPADTAINAEGQGS 422
Db 377 LRRRHFKGDYSTKKHVGNGYSKAGIPQHPHMAQNLQVPDDSDDEKKA--SPLGSS 434
QY 423 GGDCKE 429
Db 435 YEEBEE 441

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RESULT 8

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ID OPCM_CHICK STANDARD; PRT; 337 AA.
AC Q98892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAR-2004 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Opioid binding protein/cell adhesion molecule homolog precursor
DE (Neurite inhibitor GP55-A) (OBAM protein gamma isoform).
GN OPCM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P.; Kim D.-S.; Howard M.R.; McNamee C.J.; Smith N.; Moss D.J.;
RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBAM cDNAs from
RT chick: structural diversity of IGLON family proteins.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A.; Kim D.-S.; Clarke G.A.; Marshall-Clarke S.; Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBAM,
RT neurotrophin, LAMP and CEPU-1.";
RL J. Cell Sci. 109:3129-3138(1996).
CC -!- FUNCTION: Inhibits neurite outgrowth.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -!- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; Y08170; CAB41420.1; -.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; Igc2; 2.
CC PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
KW Membrane; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 314
FT PROPEP 315 337 MOLECULE BINDING PROTEIN/CELL ADHESION
FT DOMAIN 32 119 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 129 211 IG-LIKE C2-TYPE 1.
FT DOMAIN 215 302 IG-LIKE C2-TYPE 2.
FT DISULFID 50 108 IG-LIKE C2-TYPE 3.
FT DISULFID 150 194 POTENTIAL.
FT DISULFID 236 288 POTENTIAL.
FT LIPID 314 314 GPI-anchor amidated asparagine
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;

Query Match 10.0%; Score 225.5; DB 1; Length 337;
Best Local Similarity 25.4%; Pred. No. 6.7e-09;
Matches 84; Conservative 57; Mismatches 139; Indels 51; Gaps 14;

QY 73 TVVAGGTIVLKQVCKDHDSLSQWNPAAQQLTYFGEKRALDRNIQLVTSPPHELSSIS 132
Db 39 TVRQGESATLRCTVDDRV-RRVAWLN-RSTLVAGNDKNSIDNRVILSTKTQYSIKIH 96
QY 133 NVALADEGEYTCSTFTMPVTRAKSLVTLGIPQKPIITGYKSSLRKDTATLNCQSSGSK 192
Db 97 NVDVDEGPTCVQTDNDHPKTSRVHLIVQVPPQIVNISSDITVNEGSSVTLCLAFG-R 155
QY 193 PAARLTWRKGDQELHGEPTRIQDPNGKFTFVSSSVTFQ---VTRDDGASIVCSVNHES 249
Db 156 PEPTVTWR---HLSGK-----GQGF-VSEDEYLEITGITREGSGEYCSAVNDVA 201
QY 250 LKADASTSORIEVLYTPTRAMIRPDPPH-----PREGQKLLHCEGRGNVPQOYLW 301
Db 202 VPDVRK---VKVTVNY-----PPYISNAKNTGASVGQKGILOCEASAVPV-AEFQW 248
QY 302 EKE-----GSVPPLKMTQE---SALIFFPLNKSDSGTYGCTATSNMGYSKAYVTLVNDP 353
Db 249 FKEDTRLANGLEGVRIESKGRSLTLTFFNVSEKDYNTVCTVANKLGTNA--SIIYGP 306

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CC CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC CC -----
DR EMBL; D86043; BAA12974.1; -
DR EMBL; Y10375; CAA71403.1; -
DR EMBL; Y11047; CAA71944.1; ALT_INIT.
DR EMBL; AB023430; BAA87929.1; -
DR EMBL; AC004832; AAF19260.1; -
DR EMBL; AL034562; CAB38674.1; -
DR EMBL; AL049634; CAB46662.1; ALT_SEQ.
DR EMBL; AL117335; CAC12723.1; -
DR EMBL; BC026692; AAB26692.1; -
DR EMBL; BC033092; AAB33092.1; -
DR EMBL; BC038510; AAB38510.1; -
DR EMBL; JCS287; JCS287.
DR Genew; HGNC:9662; PTPNS1.
DR MIM; 602461; -
DR GO; GO:0005886; C:plasma membrane; TAS.

Query Match 10.5%; Score 238.5; DB 1; Length 503;
Best Local Similarity 24.2%; Pred. No. 1.4e-09;
Matches 110; Conservative 71; Mismatches 152; Indels 121; Gaps 23;

QY 8 LLLLLLACWAPGGANLSDQGYWQEDLEGLTAPLDEAISTVWSPDMLASQDSQP 67
DB 14 LCLLLAASCAWS-----GVAGEELQV--IQP-DKSVS-----44
QY 68 WTSDETVVAGTVLKVQKVDHEDSL-----QW---SNPAQOTLYFGEKRALRNRQ 118
DB 45 -----VAGESAILHCTV-----TSLIPVGPQIWFGRGAGFARELIY-NQKEGHFRVTT 92
QY 119 LMTSTPE---LSSISNVALDEGEVTCISF-----TMPVTKSLVTLVGLPKPPII 169
DB 93 VBSSTKRENDFDISISNITTPADAGTYCVKFKGSPDTFEKSGAGTELSVRAKPAVV 152
QY 170 TGYKSLREKDTATLNCQSSGSKPA-ARLTWRKGDQELHGEPTRIQEDPNKG--TFTVS 226
DB 153 SGPAARATPQHTVFTCESHGFSFPRDITLKWFKNGNELSDFQTNV--DPVGESVSVSIHS 210
QY 227 SVTFQVTRDDGASIVCSVNHESLKGAD-RSTQRIEVLVYPTAMIRPDPPHREGOKLL 285
DB 211 TAKVLTREDVHSQVCEVAHVTLQSDPLRGNTLSETIRVPTPLEVTQOPVRAEQ-VN 269
QY 286 LHCEGRG-NPVPQYLWEKGSVPPLKMTQESALIFPFLNKSQSGTGTATSNMGSYKA 344
DB 270 VTCQVRKFYQRLQTLWLENGV---SRTASTV-----TENKDGTY-----NWMS 313
QY 345 YTYTLNV-----NDPSPVPS-----SSSTVHAIGG-----I 370
DB 314 WLLVNVSAHRDDVKLTQCVHEHDGQPAVSKSHDLKVSAPHKPEQSGNTAENTGSGNERIYI 373
QY 371 VARTVFLILLMLTFLGHLVLRHKGTYLTHKAGS 404
DB 374 WGVGVCTLLVALLMAALVYLVRIR-----OKKAQGS 403

RESULT 7
PVRI_MOUSE STANDARD; PRT; 515 AA.
AC Q9JUF6; Q9JUL5; Q9JUL7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (hvec) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
RA Lecocq E., Dubreuil P., Campadelli-Piume G.;
RT "The murine homolog of human nectin delta serves as a species
RT non-specific mediator for entry of human and animal alpha herpesviruses
RT in a pathway independent of detectable binding to gp. ";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha
RT (Hvec) in sequence and activity as a glycoprotein D receptor for
RT alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the
RT floor plate during embryogenesis, suggesting a role in neural
RT development. ";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INFO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gpD).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF239762; AAF60333.1; -
DR EMBL; AF270977; AAF76195.1; -
DR EMBL; AF297665; AAG22808.1; -
DR MGD; MGI:1926483; Pvr1l.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 354 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 355 375 POTENTIAL.
FT DOMAIN 376 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 436 442 POLY-GLU.
FT DOMAIN 443 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

RX MEDLINE=97215901; PubMed=9062191;
RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ullrich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase
RT receptors";
RL Nature 386:181-186(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
RP ARG-107; GLY-109 AND VAL-131.
RC TISSUE=Monocytes;
RX MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells";
RL Eur. J. Immunol. 28:1-11(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
RP VAL-131.
RC TISSUE=Brain;
RX MEDLINE=20053880; PubMed=10585853;
RA Sano S.-I., Ohnishi H., Kubota M.;
RT "Gene structure of mouse BIT/SHPS-1";
RL Biochem. J. 344:667-675(1999).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,
RA Hammond S., Harley J.B., Heath F.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20";
RL Nature 414:865-871(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
RP GLY-109 AND VAL-131.
RC TISSUE=Brain, Kidney, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B.
RX MEDLINE=99401000; PubMed=10469599;
RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
RA Schraven B., Neel B.G.;
RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
RT multi-protein complexes in macrophages";
RL Curr. Biol. 9:927-930(1999).
RN [8]
RP PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH PTPN11 AND JAK2.
RX MEDLINE=20428742; PubMed=10842184;
RA Stofega M.R., Argetsinger L.S., Wang H., Ullrich A., Carter-Su C.;
RT "Negative regulation of growth hormone receptor/JAK2 signaling by
RT signal regulatory protein alpha";
RL J. Biol. Chem. 275:28222-28229(2000).
RN [9]
RP FUNCTION, AND INTERACTION WITH CD47.
RX MEDLINE=21400825; PubMed=11509594;
RA Latour S., Tanaka H., Demeure C., Mateo V., Rubio M., Brown E.J.,
RA Malszewski C., Lindberg F.P., Oldenborg A., Ullrich A.,
RA Delepesse G., Sarfati M.;
RT "Bidirectional negative regulation of human T and dendritic cells by
RT CD47 and its cognate receptor signal-regulator protein-alpha:
RT down-regulation of IL-12 responsiveness and inhibition of dendritic
RT cell activation";
RL J. Immunol. 167:2547-2554(2001).
CC -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6, PTPN11 and
CC other binding partners from the cytosol to the plasma membrane.
CC Supports adhesion of cerebellar neurons, neurite outgrowth and
CC glial cell attachment. May play a key role in intracellular
CC signaling during synaptogenesis and in synaptic function (By
CC similarity). Involved in the negative regulation of receptor
CC tyrosine kinase-coupled cellular responses induced by cell
CC adhesion, growth factors or insulin. Mediates negative regulation
CC of phagocytosis, mast cell activation and dendritic cell
CC activation. CD47 binding prevents maturation of immature dendritic
CC cells and inhibits cytokine production by mature dendritic cells.
CC -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC Binds FGR (By similarity). Binds JAK2 irrespective of its
CC phosphorylation status and forms a stable complex. Binds SCAP1
CC and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P78324-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P78324-2; Sequence=VSP_007030;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=P78324-3; Sequence=VSP_007029;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
CC Detected on myeloid cells, but not T cells. Detected at lower
CC levels in heart, placenta, lung, testis, ovary, colon, liver,
CC small intestine, prostate, spleen, kidney, skeletal muscle and
CC pancreas.
CC -!- PTM: N-glycosylated.
CC -!- PTM: Phosphorylated on tyrosine residues in response to
CC stimulation with EGF, growth hormone, insulin and PDGF.
CC Dephosphorylated by PTPN11.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.

CC CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930_g.htm".

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CC CC or send an email to license@isb-sib.ch).

CC CC -----

DR ENBL; X76400; CAA53980.2; ALT_INIT.

DR ENBL; AF060231; AAC23798.1; -.

DR ENBL; AY029539; AAK33124.1; -.

DR ENBL; AF252867; AAG16648.1; -.

DR ENBL; AF196768; AAG16648.1; JOINED.

DR ENBL; AF196769; AAG16648.1; JOINED.

DR ENBL; AF196770; AAG16648.1; JOINED.

DR ENBL; AF196771; AAG16648.1; JOINED.

DR ENBL; AF196774; AAG16649.1; -.

DR ENBL; AF196768; AAG16649.1; JOINED.

DR ENBL; AF196769; AAG16649.1; JOINED.

DR ENBL; AF196770; AAG16649.1; JOINED.

DR ENBL; AF196771; AAG16649.1; JOINED.

DR ENBL; AF196772; AAG16649.1; JOINED.

DR ENBL; AF196773; AAG16649.1; JOINED.

DR GENE; HGNC:9706; PVRL1.

DR MIM; 600644; -.

DR MIM; 225000; -.

DR MIM; 225060; -.

DR GO; GO:0016021; C:integral to membrane; NAS.

DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.

DR GO; GO:0015026; F:coreceptor activity; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 2.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00835; IG-LIKE; 2.

KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

KW Repeat; Glycoprotein; Signal; Alternative splicing.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 517 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.

FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 356 376 POTENTIAL.

FT DOMAIN 377 517 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 31 141 IG-LIKE V-TYPE.

FT DOMAIN 149 238 IG-LIKE C2-TYPE 1.

FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.

FT DOMAIN 437 444 POLY-GLU.

FT DOMAIN 445 449 POLY-GLY.

FT DISULFID 51 124 BY SIMILARITY.

FT DISULFID 172 226 BY SIMILARITY.

FT DISULFID 269 316 BY SIMILARITY.

FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).

FT VARSPLIC 335 352 EFPYTPSPPEGRAGPV -> AFCQLYFGKGRTRMFM

FT (in isoform Gamma).

FT Missing (in isoform Gamma).

FT VARSPLIC 353 517 /FTid=VSP_002625.

FT VARSPLIC 336 458 ALRRRHTFKGDYTKKHVYNGSKAGIPQHHPMAQNLO

FT YPDSDDKKAGPLGGSSSEEEEEEGGGGGRKVGPH

FT -> KRPQFGGLSARLAVTLVAVLIVFFLYNRQ

FT QKSPETDAGTDPLSOKPEPSRQSLVPEDIQVHLD

FT PGRQQQEEEDLOKSLQPPYDILGVSPSYHPSVRRTEPRG

FT ECP (in isoform Alpha).

FT VARSPLIC 459 517 /FTid=VSP_002626.

FT Missing (in isoform Alpha).

FT /FTid=VSP_002627.

SQ SEQUENCE 517 AA; 57158 MW; DF34C8AEC93BE6D CRC64;

Query Match 10.6%; Score 239; DB 1; Length 517;

Best Local Similarity 26.8%; Pred. No. 1.3e-09;

Matches 114; Conservative 52; Mismatches 161; Indels 98; Gaps 24;

QY 77 GTTVLTKCQVKDEHS-----SLQWS-----NPAQOTLYFGKRALRDNRQL 119

DB 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPMSGVSLAYPR-----ERVDF 99

QY 120 VTSTPHELISISNVALADEGYTCISFTMPVVRTAKSLVTLVILGIPQKPI--ITGYKSSLR 177

DB 100 LRPSFTDGTIRLSRLEDEGVVICEFATFTGNRESQLN-LTVMAKPTNWIEGTQAVLR 158

QY 178 EK---DTATL--NCQSSGSKPAARLTWRKGDDELHCEPRIOE--DPNGKTFVTSSSVTF 230

DB 159 AKKGQDDKVLVATCTSAANGKPPSVWSW---ETRLKGE-AYEQEIRNPNG-TVTVISRYRL 213

QY 231 QVTRDDGASIVCSVNHSILKGADR-STSORIEVLYTPTAMIRP-DPPHREGQKLLIHC 288

DB 214 VPSREAHQOSLACIVNYH---MDRFKESLTLNVOYEPEVTIEGFGNWLQEMDKVLTC 269

QY 289 EGRGNVPQOYLWEK-EGSVPLPKMTQESALIPFP-LNKSDSGTYCTATSNNGSKYAY 346

DB 270 KADANPPATEYHWTTLNGLSPKGVAAQNRTLPKGPINYSAGTYICEATNPIGTRSGQV 329

QY 347 TLNVND-----PS-----PVPSSSYTHAIGGIVAFIVFELLIMLIFLGHYLI--- 390

DB 330 EVNITEFPYTPSPPEHRRAGPVPT-----AIIQGVAGSI-----LLVLIVVGIVVALR 379

QY 351 --RH--KGTVLT-----HEAKGSDDAPDADTAIINAEGGOSGG 424

DB 380 RRHRTFGDYSTKHYVNGYSKAGIPQHHPMAQNLOYPDDSDDEKKA--GFLGSSSYE 437

QY 425 DDKKE 429

DB 438 EEEEE 442

RESULT 6

SHSI_HUMAN STANDARD; PET; 503 AA.

ID P78324; O00683; O43799; Q8N517; Q8TAL8; Q9H022; Q9UDX2; Q9UIJ6;

AC Q9V4U9;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor

DE (SHP substrate-1) (SHPs-1) (inhibitory receptor SHPS-1) (Signal-

DE regulatory protein alpha-1) (SHP-alpha-1) (SHP-alpha-2) (SHP-alpha-

DE 3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based

DE activation motifs) (Bit) (Macrophage fusion receptor) (p84).

GN PFNSI OR SHPSI OR SIRP OR MID1 OR BIT OR MFR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=97223399; PubMed=9070220;

RA Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,

RA Fujioka Y., Kasuga M.;

RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal

RL localization of genes.";

RN Blochem. Biophys. Res. Commun. 231:61-67 (1997).

RP [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION,

RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTFN11, PTFN6 AND GRB2.

RC TISSUE=Placenta;

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EMBL: AF308632; AAC30281.1; --
DR HSP: P06907; INEU
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLU.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 11.1%; Score 250.5; DB 1; Length 515;
Best Local Similarity 26.9%; Pred. No. 2e-10;
Matches 116; Conservative 54; Mismatches 157; Indels 105; Gaps 25;

QY 77 GGTIVLKKQVKDH-----EDSSLOW-----NPAQQLYFGKRALDRNRQL 119
DB 44 GTDVLHCFANPLPGVKITQVTWQKATNGSKQVAINPAMGVSLAPYR-----ERVEF 99
QY 120 VTSTPHELSTISINVALADEGYTCISFTMPVPTAKSLVTLVGIPOKPI---ITGYKSLR 177
DB 100 LRPSFTDGTIRLSRLLEDEGVYICFATFPAGNRSQLN-LTVMKPTNWTGTOAVLR 158
QY 178 E---KDTATL--NCQSSGSKPAARLTWRKQDELHGEPTRIQE--DPNGKTFVTSSSVTF 230
DB 159 AKGKDKKVLVATCTSANGKPPSVSN---ETHLKE-AYEQIRNPNG-TVTVISRYRL 213
QY 231 QVTREDDGASIVCSVNHSKLGADR-STQRIEVLTYPTAMIRP-DPPHPREQKILLHC 288
DB 214 VPSREDHQSLACIVNH-----MDRFRESLTNLVQVEPEVTIEGFGNMYLQRMVVKLAC 269
QY 289 EGRGNFVPOQYLWEK-EGSVPLPKMTQBSALIF--PFLNKSDSGTIGCTATSNMGSKYKAY 345
DB 270 KADANPPATEYHWTTLNGLSLFKGVQAEQNTLFFRGP-INYSMAGTYICATNPIGTRSGQ 328
QY 346 YTLNVND-----PSP-----VPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLI-- 390
DB 329 VEVNITEFPYTPPEHGRAGQVPT-----AIIQGVGSI-----LLVLVVGVGVVAL 378
QY 391 ---RH--KGYLTHE-----AKGSDP-----APDADTAIIN 416
DB 379 CRRRHTFKGDYSTKHHVYNGVSKAGIPQHPHPPMAQLQVPEDSDDEKKAGLGGSSYEE 438
QY 417 AEGGQSGGDDKK 428
| : | : | : |

Db 439 EBEEGGGGERK 450

RESULT 5

PVRL1_HUMAN

ID PVRL1_HUMAN STANDARD; PRT; 517 AA.

AC Q15223; O75465; O9HB36; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
(CD111 antigen).
GN PVRL1 OR PRR1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "cDNA characterization and chromosomal localization of a gene related
to the poliovirus receptor gene.";
RL Gene 155:261-265(1995).
RN [2]
RX SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127;
RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
protein 1 and poliovirus receptor.";
RL Science 280:1618-1620(1998).
RN [3]
RX SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
RA Campadelli-Fiume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
nectin1 (or prr1-HIGR-HvEC) modulates positively and negatively
susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691(2001).
RN [4]
RX SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=20392396; PubMed=10932188;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RA Helms J.A., Spritz R.A.;
RT "Mutations of PVRL1, encoding a cell-cell adhesion
molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
dysplasia.";
RL Nat. Genet. 25:427-430(2000).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoform gamma).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=Delta;
IsoID=Q15223-1; Sequence=Displayed;
Name=Alpha;
IsoID=Q15223-2; Sequence=VSP_002626, VSP_002627;
Name=Gamma;
IsoID=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
responsible for allelic forms known as Margarita Island ectodermal
dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);

FT		ATGLGP -> DTPOASRDVGLVMGAVGGTLLVLIIAGGFL	
FT		AllILRRRRRSKPGSGNDGRGSVDPKTOVFNGGPGPVFW	
FT		RSASPMPRPGRDEDEEBEEMKAEGMLPPHSPKDDM	
FT		ESHLDGSLISRAIV (in isoform Alpha).	
FT		/FTID=VSP_002630.	
FT	VARSPLIC	468 530 Missing (in isoform Alpha).	
FT		/FTID=VSP_002631.	
SQ	SEQUENCE	530 AA; 57317 MW; 0ED71BFÅ2B231BBE CRC64;	
QY	Query Match	11.3%; Score 256; DB 1; Length 530;	
Dd	Best Local Similarity	24.4%; Pred. No. 8.6e-11;	
Dd	Matches 100; Conservative	52; Mismatches 160; Indels 98; Gaps 16	
QY	3 APAASILLLLLIFACCCWAPGCANLSODGYMOEQDLEL-----GT-----LAP 44		
Dd	13 SPITLPPLPLLLL-----LQETG---AQDVRVLVPEVRGRLGCTVELPCHLPPP 59		
QY	45 LDEAISVTWNSSPDMLASQSDQPWTSDETVVAGGTVVKCVKDHESSLOWSNPAOQTLL 104		
Dd	60 TTERVSQVTTWORLD-----GTVV-----AAFHPSGVDFFN----- 90		
QY	1C5 YFGEKRALNRNLQLVSTP-----HELISISINVALADEGETYCSIFTVPRTAKSLV 158		
Dd	91 -----SOPFSKDRLSFVARPETNADRLATLAFRGLRVEGNTYCFATFPNGTRRG-V 144		
QY	159 TVLGIPOKP--IITGYKSSIREKDTALNCQSSGSKFAARLTWRKKDQELHGEPTRIQED 216		
Dd	145 TWLRVIAQENHAEAQEVITIGPSVAVARCVSTGGRPARITW---TSSLGEAKDTQEP 201		
QY	217 P-NGKTPVSSVTFQVTRDDGASIVCSNVNHESLKGAADRSTQSRIEVLTYPTAMIRDPD 275		
Dd	202 GIOAGVTIIISRYSLVPVGRAADGVKVTCRVEHSFEE-----PILLPVLTLVSRYEP 252		
QY	276 PHREG-----OKLLIHCEGRGNPFVQQYLWE-KESGVPPLKMTORSEALLFPFLNK 325		
Dd	253 EVISIGYDDNWYLCGRSAILLTCVDRNSEPTDYDMSTTGTFPASAVAQSQLLVHSVDR 312		
QY	326 SDSGTGYCTATSNMGSKAYITLVNNDPSPVPSSSYTHAIIGGIVAFIV 375		
Dd	313 MVNTTICTATNAVGTGRAQVILVRE-SPTAGAGATGGHIGLIAAIL 361		
RESULT 4			
PVRI_PIG			
ID	PVRI_PIG	STANDARD;	PRT; 515 AA.
AC	Q9GL76;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).		
DE	PVRL1 OR PRRI OR HVEC.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_Taxid=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21176378; PubMed=11277703;		
RA	Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;		
RA	"Porcine HveC, a member of the highly conserved HveC/nectin 1 family,		
RT	is a functional alphaherpesvirus receptor.";		
RL	Virology 281:315-328(2001).		
CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.		
CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gp) (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.		
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.		
CC	This SWISS-PROT entry is copyright It is produced through a collaboration		

DR EMBL; X64118; CAA45478.1; JOINED.
 DR EMBL; X64119; CAA45478.1; JOINED.
 DR EMBL; X64120; CAA45478.1; JOINED.
 DR EMBL; X64121; CAA45478.1; JOINED.
 DR EMBL; X64122; CAA45478.1; JOINED.
 DR EMBL; X64123; CAA45478.1; JOINED.
 DR EMBL; X64116; CAA45479.1; JOINED.
 DR EMBL; X64117; CAA45479.1; JOINED.
 DR EMBL; X64118; CAA45479.1; JOINED.
 DR EMBL; X64119; CAA45479.1; JOINED.
 DR EMBL; X64120; CAA45479.1; JOINED.
 DR EMBL; X64121; CAA45479.1; JOINED.
 DR EMBL; X64122; CAA45479.1; JOINED.
 DR EMBL; X64123; CAA45479.1; JOINED.
 DR EMBL; X64116; CAA45480.1; JOINED.
 DR EMBL; X64117; CAA45480.1; JOINED.
 DR EMBL; X64118; CAA45480.1; JOINED.
 DR EMBL; X64119; CAA45480.1; JOINED.
 DR EMBL; X64120; CAA45480.1; JOINED.
 DR EMBL; X64121; CAA45480.1; JOINED.
 DR EMBL; X64122; CAA45480.1; JOINED.
 DR EMBL; X64123; CAA45480.1; JOINED.
 DR EMBL; AC068948; AAF69803.1; --
 DR PIR; A43024; RWHUPD.
 DR PIR; S12048; RWHUPA.
 DR Genew; HGNC:9705; PVR.
 DR MIM; 173850; --
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007125; P:invasive growth; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 Repeat; Antigen; Alternative splicing; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT POTENTIAL
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 218 218
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPPLIC 340 384
 FT VARSPPLIC 331 331
 FT VARSPPLIC 332 384
 FT VARSPPLIC 385 392
 FT VARSPPLIC 393 417
 FT VARIANT 67 67
 FT VARIANT 340 340
 FT SEQUENCE 417 AA; 45302 MW; D15C013CE853169B CRC64;

Query Match 11.6%; Score 263; DB 1; Length 417;
 Best Local Similarity 25.7%; Pred. No. 2e-11;
 Matches 108; Conservative 50; Mismatches 158; Indels 104; Gaps 17;
 QY 5 AASLLLLLLFACWACGAGANLSQGYWQEQDLELGTILAPLDEAISTVWSSPDMLASQD 64
 DB |||||
 QY 65 SQTPTSDETVVA-----GGTVVLKC--QVKDHE--DSSLOWSNPAQOTLYFGEKRA 111
 DB |||||
 QY 24 --PGTGVVWVQAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWAR-----HGEGSG 74
 DB |||||
 QY 112 L-----RDNRILQVTSFPEHLSISISNVAL-----ADSEGYTCSTFTMPVR 152
 DB |||||
 QY 75 MAVFHTQGPSYSESKLEFVAA---RLGAELRNASLRMPGLRVEDEGNYTCLFVTFP-Q 130
 DB |||||
 QY 153 TAKSLTVVLGIPQKIITG--YKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHCEP 210
 DB |||||
 QY 131 GSRSDIWLRLVLAKEPQNTAEVQKVLGEPVPMARCVSTGGRPPAQITWH---SDLGMP 187
 DB |||||
 QY 211 TRIOEDPN--GKTFVSSSVTFQVTRDDGASIVCSVNHSLKGAADSTSORIEVLYTPT 268
 DB |||||
 QY 188 NTSQV-PGFLSGTVTVTSILWLPSSQVDGKNVTCKVEHSEFEPQLLT-VNLTVYYPE 245
 DB |||||
 QY 269 AMIRPDPPHPREGQ-KLLHCEGRGNPVPQOYLWEKE-GSVPPKMTQESALIFPPFNKS 326
 DB |||||
 QY 246 VSIQYDNNWYLGQNEATLTCDAENPEPTGYNNWSTMTGMLPPFAVAGQAQLIRPYDKP 305
 DB |||||
 QY 327 DSGTYGCTATSNMGSKYKAYTYLNNPSPVSSSTYHAIIGTVAFIVFLLIMLIFLG 386
 DB |||||
 QY 306 INTTLICNVNTALGARQAEITVQKGPSPSEHSGISRNALI-----FLVLGLVFLILG 360
 DB |||||
 RESULT 3
 PVR2_MOUSE
 ID PVR2_MOUSE STANDARD; PRT; 530 AA.
 AC P32507; Q62096;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
 entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
 GN PVRL2 OR PVS OR PVR OR MPH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=92219365; PubMed=1560525;
 RA Morrison M.E., Racaniello V.R.;
 RT "Molecular cloning and expression of a murine homolog of the human
 poliovirus receptor gene.";
 RL J. Virol. 66:2807-2813 (1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=C57BL/6; Tissue=Brain;
 RX MEDLINE=94179228; PubMed=8132569;
 RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
 RT "Amino acid residues on human poliovirus receptor involved in
 interaction with poliovirus.";
 RL J. Biol. Chem. 269:8431-8438 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=FVB/N; Tissue=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

```

DR PROSITE; PS0835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT TRANSMEM 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 85 85
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VARSPLIC 386 392
FT VARSPLIC 393 417
FT VARSPLIC 417 417
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6B1F CRC64;

Query Match      12.0%; Score 272; DB 1; Length 417;
Best Local Similarity 26.2%; Pred No. 4.5e-12;
Matches 106; Conservative 56; Mismatches 183; Indels 60; Gaps 16;

QY 67 PWTSDETVVA-----GGTVVLKC--QVKDHD-----SSIQSNPAQ-----QT 103
Db 24 PGTGDIIVQAPTQVPGFLGDSVTLPCVLQVPGMEETHVSLQTSRHGSGSMVAFHQTQ 83

QY 104 LYFGEKALDRNRQLQVTSFHELSISISVALADEGEYTCSTFTMPVRAKSLVTVGI 163
Db 84 PNYSEPKRLEFVAARLGTTEL-RDASLRFGLRVEDEGNYTCLFTFP-QGSRSDVILWRV 141

QY 164 PQKPIITG--YKSLREKDTATLNCQSSGSKPAARLTWRGQDLHGEPTRIQEDPN--G 219
Db 142 LAKPONTAEQVKVQLTKGKPVKARCVSTGGRPPAHITWH---SDLGMPNTSQA-PGFLS 197

QY 220 KTFVTSSSVTFQVTRDDGASIVCSNVHESLKGADRTSQRIEYLYTPTAMIRP-DPPHP 278
Db 198 GTVTVTSLIILVPSQVDGKSVTKVHESPEKQLLT-VNLTVYYPEVSIQSYDNNWY 256

QY 279 REGOKLLIHCEGRNPVPQVLYEKE-GSVPLPKMTQESALIPFLNKSQSGTYGCTATS 337
Db 257 LSQNEATLTCDARENPEPTGYNWSTTNGPLPFPFAVAQGLLRVPDKPINTTFCNVTN 316

QY 338 NMGSYKAYTINVND-PSVPSSSTYHAIIGGIVAFIVFLLIMLIFLG----- 386
Db 317 ALGARQAEIVQVKEGPPSPSGMSS-----NIIIFLIGVILLTLLGIGVYFYSRC 370

QY 387 -----HYLRHKGTVLTHKAGSDPADPADPAINAEQGQSG 424
Db 371 SREFLWCHLSPSSEEHASASANGYISYSDVSREASSQDPQTEG 415

RESULT 2
PVR_HUMAN
ID PVR_HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89188426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
sequence, and expression of a new member of the immunoglobulin
superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=91060015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
and secreted forms.";
RL EMBO J. 9:3217-3224(1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyanni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a 1mb region in 19q13.2 containing a zinc finger
gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N Glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS.
CC Event-alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24407; AAA36461.1; -
CC EMBL; M24406; AAA36462.1; -
CC EMBL; X64116; CAA45478.1; -
CC EMBL; X64117; CAA45478.1; JOINED.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 9.17522 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187b-8
Perfect score: 2364
Sequence: 1 MGAPASLLLLLLLACFWA.....ALINAEQGSGDDKKEYFI 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	12.0	417	1	PVR_CERAE
2	263	11.6	417	1	PVR_HUMAN
3	256	11.3	530	1	PVR2_MOUSE
4	250.5	11.1	515	1	PVR1_PIG
5	239	10.6	517	1	PVR1_HUMAN
6	238.5	10.5	503	1	SHS1_HUMAN
7	228.5	10.1	515	1	PVR1_MOUSE
8	225.5	10.0	337	1	OPCM_CHICK
9	225.5	10.0	538	1	PVR2_HUMAN
10	225	9.9	338	1	LAMP_CHICK
11	220.5	9.7	348	1	KILO RAT
12	217.5	9.6	506	1	SHS1_BOVIN
13	217.5	9.6	583	1	C166_MOUSE
14	216.5	9.6	702	1	CEA5_HUMAN
15	215	9.5	739	1	VCAL_RAT
16	212.5	9.4	583	1	C166_HUMAN
17	212	9.4	4391	1	PGEM_HUMAN
18	208	9.2	345	1	OPCM RAT
19	207	9.1	345	1	OPCM_HUMAN
20	206	9.1	345	1	SHS1_RAT
21	205.5	9.1	338	1	LAMP_RAT
22	205	9.1	338	1	LAMP_HUMAN
23	205	9.1	344	1	NTRI_HUMAN
24	204	9.0	513	1	SHS1_MOUSE
25	203	9.0	345	1	OPCM_BOVIN
26	198.5	8.8	353	1	CEPU_CHICK
27	197.5	8.7	547	1	ICAZ_HUMAN
28	197	8.7	344	1	NTRI_MOUSE
29	196	8.7	344	1	NTRI RAT
30	196	8.7	3707	1	PGEM_MOUSE
31	192.5	8.5	1051	1	PTK7_CHICK
32	192.5	8.5	1447	1	DCC_MOUSE
33	191.5	8.5	1443	1	NEOI_CHICK

RESULT 1

PVR_CERAE

ID	PVR_CERAE	STANDARD	PRT	417 AA
AC	P32506			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Poliovirus receptor precursor.			
GN	PVR OR PVS.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Rutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).			
RC	TISSUE=Kidney;			
RX	MEDLINE=93059651; PubMed=1331508;			
RA	Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;			
RT	"A second gene for the African green monkey poliovirus receptor that has no putative N-glycosylation site in the functional N-terminal immunoglobulin-like domain.";			
RL	J. Virol. 66:7059-7066(1992).			
CC	-I- FUNCTION: Not known. Used by poliovirus to bind and enter the cell.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).			
CC	Secreted (isoforms beta and gamma).			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=4;			
CC	Name=Alpha;			
CC	IsoId=P32506-1; Sequence=Displayed;			
CC	Name=Beta;			
CC	IsoId=P32506-3; Sequence=Not described;			
CC	Name=Gamma;			
CC	IsoId=P32506-4; Sequence=Not described;			
CC	Name=Delta;			
CC	IsoId=P32506-2; Sequence=VSP 002622; VSP 002623;			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like_v-type domain.			
CC	-I- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; D12611; BAA02136.1; -			
DR	EMBL; D12612; BAA02137.1; -			
DR	PIR; A44194; A44194.			
DR	PIR; B44194; B44194.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 3.			
DR	SMART; SM00406; IGV; 1.			

Job time : 14.4885 secs

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Db 474 AEDTGKALVCLAKLHSSQSEPKQKQSTQTLVYNNAPKEPTIWVSPSPV-PEEGSPVNL 532
Qy 287 HCEGRGNEVPQOYLWE---KEGSVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSK 343
Db 533 TCSSDGFPTP-KILWSRQLKNGELQPL--SQNTTSLFMAWKMEDSGIYVCEGINEAGISK 589
Qy 344 AYYTLNVNDPS-----PVPSSSTYHAIIG--GIVAFIVFL-----LIMLIF 384
Db 590 KVELLIQGGSKDIQLTVFPKSKVKEGDTVIISCTCGSVPEIWIILKKAKTGDWVLKSV 649
Qy 385 LGHYLIR-----HKGTY-----LTHEAKGSDDAPD-----ADTAI 414
Db 650 NGSTYIRKAQLQDAGVCECKTEVGSQLSRLTLDVKGKNNKDYFSPPELLALYFASSLV 709
Qy 415 INAEG 419
Db 710 IPAIG 714

RESULT 15
153960
PRR2 alpha - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I53960
R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I53960
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-478 <RES>
A:Cross-references: GB:S79171; NID:g1042202; PID:g1042203
C:Genetics:
A:Gene: PRR2alpha
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 9.4%; Score 213.5; DB 2; Length 478;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
Matches 89; Conservative 55; Mismatches 167; Indels 81; Gaps 16;

Qy 77 GGTVVLKQV-----KDHED-----SSLOWNPAAQOTLYF- 106
Db 47 GGTVELCHLLPPVPGLYISLVTWQRDAPANHQNVAAFHFKMGPSFPSPKPGSERLSFV 106
Qy 107 -GEKRALRDNRIQLVSTPHELISISINVALADEGEVTCSTFTMPVRTAKSLVTLGIPQ 165
Db 107 SAKQSTGQDTEAEIQQDAT-----LALHGLTVEDEGNYTCFATFPKGSVRGM-TWLRVIA 160
Qy 166 KP--IITGYKSLREKDTATLNCQSSGSKPAARLTWRKQDELHCEPTRIQEDPENGKFTT 223
Db 161 KPKNQAEQAQKVTFSQDPTTVALCISKEGRPPARISW-LSSLDWEAKETQVSGTLAG-TVT 218
Qy 224 VSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAM-----RP 273
Db 219 VTSRFTLVPSGRADGVTVTCKVEHSEFE-EPALIPVTLSVRYPPEVSIQYDDNNWYLGRT 277
Qy 274 DPPHPREGQKLLHCEGRGNPVPQOYLWE-KEGSVPPLKMTQESALIFPFLNKSQSGTYG 332
Db 278 D-----ATLSCDVRNPEPTGYDWTSTGTFPTSVAQAQSQLVHVAVDSLFWNTFV 328
Qy 333 CTATSNMGSKYAYTLNVND-PSVPSSSTYHAIIGIVAFIVFLIMLIFLGHYLIR 391
Db 329 CTVTNAVGMGRAEQVIFVRETFRPRDRVGPLVWGAAGV-----TLVLVLLLAGGSL-- 379
Qy 392 HKGYLTHEAKGSDDAPDADTAIINAEQGSG 423
Db 380 ---AFILLRVRRRKSPG-----GAGGASG 402
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Search completed: May 27, 2004, 09:32:26

A:Molecule type: DNA
A:Residues: 35-141 <KHA>
R:Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A:Title: Characterization of the genomic organization of human carcinoembryonic antigen
A:Reference number: 154224; MUID:9113118; PMID:2286372
A:Accession: 154224
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: GB:M60964; NID:g180215; PIDN:AAA51964.1; PID:g180217
R:Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A:Title: Isolation and characterization of cDNA clones encoding the human carcinoembryonic antigen
A:Reference number: 159098; MUID:87204247; PMID:3033671
A:Accession: 159098
A:Status: translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 331-702 <RE2>
A:Cross-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
R:Steben, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A:Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105 KD
A:Reference number: A26831; MUID:87326349; PMID:3632664
A:Accession: A26831
A:Molecule type: protein
A:Residues: 35-64 <SIE>
R:Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A:Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at C-terminus
A:Reference number: A35490; MUID:90321257; PMID:2372297
A:Accession: A35490
A:Molecule type: protein
A:Residues: 'X', 140-151, 'X', 153, 'X', 155-156 <THO>
A:Note: This is the amino terminal end of a fragment shown to mediate uptake by Kupffer cells
C:Comment: This heavily glycosylated membrane protein of unknown function is a widely used marker for liver metastasis
C:Genetics:
A:Gene: GDB:CEA
A:Cross-references: GDB:119054; OMIM:114890
A:Map position: 19q13.2-19q13.2
A:Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatidylcholine
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-678/Domain: carcinoembryonic antigen #status predicted <MAT>
F:160-217/Domain: carcinoembryonic antigen homology <IMM1>
F:252-301/Domain: carcinoembryonic antigen homology <IMM2>
F:338-395/Domain: carcinoembryonic antigen homology <IMM3>
F:516-573/Domain: carcinoembryonic antigen homology <IMM4>
F:608-657/Domain: carcinoembryonic antigen homology <IMM5>
F:679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

Query Match 9.6%; Score 216.5; DB 2; Length 702;
Best Local Similarity 27.7%; Pred. No. 1.3e-07;
Matches 85; Conservative 36; Mismatches 135; Indels 51; Gaps 15;

QY 77 GGTIVLVKQVKHEDSLQWNPAAQTLFGKRAALRNRIQLVSTPHELISISNVAL 136
Db 430 GYNLSLSCHASNPFPQYSW-----LIDGNIQ-----QHTQELFISNITE 469

QY 137 ADGEYTCISFTMP---VFTAKSLVTLGIPQKPIITGYKSS-LRBNKDTATLNCQSSGSK 192
Db 470 KNSGLYTCQANNSASGHSRTVTKITVSAELRPSISSNNKSPVEDKDAVFCE----- 524

QY 193 PAARLT---WRKGDQELHGEPTRIQDENGKTTTVSSSVTVQVTRDDGASIVCSVNHES 249
Db 525 PEQNTTYLWVNGQSLVSP-RLQSLNGNRRLTL-----FNVTR-NDARAYVCGI--QN 575

QY 250 LKADRSQRIEVLVTP-TAMIRPDPPHPRQKLLHCEGRGNFVQOYLWEKGSVP 308
Db 250 LKADRSQRIEVLVTP-TAMIRPDPPHPRQKLLHCEGRGNFVQOYLWEKGSVP 308

Db 576 SVSANRSDPVTLDVLYGPDTPITSPDSSYLSGANLMLSCHASNPSP-QYSWRINGI-- 632
QY 309 PLKMTQESALIFPLKNSDSGTGCG---TATNMGSKYKAYTYLNVNDPSPVPSSSTYH 364
Db 633 PQOHTQ--VLFFIAKITPNNGTITACFVSNLATGRNNSIVKSTIVTSASGTSFGLSAGATVG 690
QY 365 AIIGGIV 371
Db 691 IMIGLV 697

RESULT 14
JS0675
vascular cell adhesion molecule-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 05-Nov-1999
C:Accession: JS0675; S19872; S23136
R:Hession, C.; Moy, P.; Tizard, R.; Chisholm, P.; Williams, C.; Wyse, M.; Burkly, L.; M.
Biochem. Biophys. Res. Commun. 183, 163-169, 1992
A:Title: Cloning of murine and rat vascular cell adhesion molecule-1.
A:Reference number: JS0674; MUID:92181437; PMID:1371918
A:Accession: JS0675
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-739 <HES>
A:Cross-references: GB:M84488; NID:Q207642; PIDN:AAA42332.1; PID:G207643
R:Williams, A.; Atkins, R.; Fries, J.; Gimbrone, M.A.; Cybulsky, M.I.; Collins, T.
submitted to the EMBL Data Library, February 1992
A:Description: Nucleotide sequence of rat vascular cell adhesion molecule-1.
A:Reference number: S19872
A:Accession: S19872
A:Molecule type: mRNA
A:Residues: 1-2, 'G', 4-121, 'HL', 124-165, 'N', 167-738, 'G' <WIL>
A:Cross-references: EMBL:X63722; NID:G57471; PIDN:CAA45254.1; PID:G57472
R:Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.; Collins, T.
Biochim. Biophys. Res. Commun. 214, 214-216, 1992
A:Title: Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.
A:Reference number: S23136; MUID:92305064; PMID:1377031
A:Accession: S23136
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2, 'G', 4-165, 'N', 167-738, 'G' <WIL>
C:Comment: This protein interacts with the beta-1 integrin very late antigen 4 on leukocytes
C:Genetics:
A:Gene: VCAM-1
C:Superfamily: immunoglobulin homology
C:Keywords: cell adhesion; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-739/Domain: vascular cell adhesion molecule 1 #status predicted <VAS>
F:239-293/Domain: immunoglobulin homology <IMM1>
F:328-385/Domain: immunoglobulin homology <IMM2>
F:526-581/Domain: immunoglobulin homology <IMM3>
F:676-696/Domain: transmembrane #status predicted <TRA>
F:697-715/Domain: intracellular #status predicted <INT>

QY 224 VSSSVTFQVTRDDGASIVCSVNHE-----LKGADRTSQRIEVLTYPTAMIRPDP 275
 Db 3535 --SHITINKAKLSDGGKVCRAASNAAGTSDIDLILKILVPPKIDKSNLIGNFLAIV----- 3588
 QY 276 PHREGQKLLHCHGRGNVPVQQYLWEKESVPLKMTQBSALIFPFLNK-----S 326
 Db 3589 -----ARTYLECPISGIPQP-DVIWTKNGM--DINMT-DSRVILAQNNETFGIENVQVT 3639
 QY 327 DSGTYGCTATSNMGSKYKAYTYTLNVNDP 353
 Db 3640 DQGRYCTATNRGGKASHDFSLDLVSP 3666
 RESULT 12
 T43290
 hemiscentin precursor - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
 C;Accession: T43290; T20993; T24734
 R;Vogel, B.E.; Hedgecock, E.M.
 A;Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-
 submitted to the EMBL Data Library, June 1998
 A;Reference number: Z23396
 A;Accession: T43290
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-5198 <VOG>
 A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1
 R;Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A;Reference number: Z19355
 A;Accession: T20993
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-5198 <WIL>
 A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CBSP:F15G9.4b
 A;Experimental source: clone F15G9
 R;Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A;Reference number: Z19929
 A;Accession: T24734
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-5198 <W12>
 A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CBSP:F15G9.4b
 A;Experimental source: clone T09B9
 C;Genetics:
 A;Gene: him-4; F15G9.4b
 A;Map position: X
 A;Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
 ; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1
 Query Match 9.6%; Score 217; DB 2; Length 5198;
 Best Local Similarity 24.5%; Pred. No. 1.7e-06;
 Matches 80; Conservative 57; Mismatches 124; Indels 66; Gaps 15;
 QY 55 SSPDLASQDSQPWTSDETV-----VAGTGVVLKQVCKDHEDSSLOWNPQAQTLTYFGE 108
 Db 3378 SEQDFKNVYTKPI-DETIDTPKAVAGGEIILKCPVLGNPTPTVTKR-----GD 3428
 QY 109 KRALRDRRIQVLTSTPHELSISINVALADEGYTCISFTMPVTRAKSLVT-----VLGI 163
 Db 3429 DAVPNDRSRHIV-----NNYDLKINSVTTEDAGQVSC-----IAYNEAGNLTHYAAEVIGK 3480
 QY 164 PQKPIITGYKSLREKDTATLNCSSGSKPAALTWKRGDQELHGBETRIQEDPNGKTF 223
 Db 3481 PTFVRKGNLYEVIENDTITMDCGVT-SRPLPISIFRGGKPY-LYDRVISISPDG----- 3534
 QY 224 VSSSVTFQVTRDDGASIVCSVNHE-----LKGADRTSQRIEVLTYPTAMIRPDP 275
 Db 3535 --SHITINKAKLSDGGKVCRAASNAAGTSDIDLILKILVPPKIDKSNLIGNFLAIV----- 3588

QY 276 PHREGQKLLHCHGRGNVPVQQYLWEKESVPLKMTQBSALIFPFLNK-----S 326
 Db 3589 -----ARTYLECPISGIPQP-DVIWTKNGM--DINMT-DSRVILAQNNETFGIENVQVT 3639
 QY 327 DSGTYGCTATSNMGSKYKAYTYTLNVNDP 353
 Db 3640 DQGRYCTATNRGGKASHDFSLDLVSP 3666
 RESULT 13
 A36319
 carcinoembryonic antigen precursor - human
 N;Alternate names: CEA; meconium antigen 100
 C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000
 C;Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; A26
 R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively,
 Mol. Cell. Biol. 10, 2738-2748, 1990
 A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
 A;Reference number: A36319; MUID:90258861; PMID:2342461
 A;Accession: A36319
 A;Molecule type: DNA
 A;Residues: 1-702 <SCH>
 A;Cross-references: GB:M17303; NID:G178676; PIDN:AAB59513.1; PID:G178677
 A;Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-Thr
 R;Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
 Mol. Cell. Biol. 7, 3221-3230, 1987
 A;Title: Isolation and characterization of full-length functional cDNA clones for human
 A;Reference number: A27773; MUID:88038876; PMID:3670312
 A;Accession: A27773
 A;Molecule type: mRNA
 A;Residues: 1-702 <BEA>
 A;Cross-references: GB:M29540; NID:G180222; PIDN:AAA51967.1; PID:G180223
 R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
 Genomics 3, 59-66, 1988
 A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
 A;Reference number: A31037; MUID:89122014; PMID:3220478
 A;Accession: A31037
 A;Molecule type: mRNA
 A;Residues: 1-702 <BAR>
 A;Cross-references: GB:M29540; NID:G180222; PIDN:AAA51967.1; PID:G180223
 A;Note: the authors translated the codon GTG for residue 130 as Leu
 R;Oikawa, S.; Nakazato, H.; Kosaki, G.
 Biochem. Biophys. Res. Commun. 142, 511-518, 1987
 A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
 A;Reference number: A25845; MUID:87128144; PMID:3814146
 A;Accession: A25845
 A;Molecule type: mRNA
 A;Residues: 5-702 <OIK>
 A;Cross-references: GB:M15042; NID:G180198; PIDN:AAA51963.1; PID:G180199
 R;Oikawa, S.
 submitted to the EMBL Data Library, September 1989
 A;Reference number: S08106
 A;Accession: S08106
 A;Molecule type: mRNA
 A;Residues: 5-319,321-702 <OIK>
 A;Cross-references: EMBL:X16455; NID:G29854; PIDN:CAA34474.1; PID:G825638
 R;Barnett, T.
 submitted to the EMBL Data Library, September 1991
 A;Description: Genomic DNA sequence upstream of the translational start of the carcinoem
 A;Reference number: S31737
 A;Accession: S31737
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-141 <BA2>
 A;Cross-references: EMBL:X62151
 R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A;Title: Identification of three new genes and estimation of the size of the carcinoembr
 A;Reference number: A44476; MUID:93052339; PMID:1427854
 A;Accession: A44476
 A;Status: preliminary; not compared with conceptual translation

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Db      100 LRPSFTDGTIRLRLELEDEGVYICEFATPTTGNRESQLN-LTVWAKPTNWIETQAVLR 158
Qy      178 EK---DTATL--NCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNG--KTFTVSSSVTF 230
Db      159 AKKGQDDKVLVACTTSANGPPSVSW---ETRLKGE-ARVPGDSGTMPMAPVTVISRYRL 214
Qy      231 QVTRDDGASIVCSVNHESLKGADR-STSORIEVLYTPTAMIRP-DPPHPREGOKLLIHC 288
Db      215 VPSREAHQQLACIVNVH---MDRPKESLTNLNVQVEPEVTIEGFDGNGWYLQRMDEVKLT 270
Qy      289 EGRGNVPVQOYLNEK-EGSVPPPLKMTQESALIPFF-LNKSDSGTYGCTATSNMGSKYAY 346
Db      271 KADANPPATEYHWTLLNGSLPKGVEAQNRYLFFKGPINYSLAGTYICEATNPIGTRSGQV 330
Qy      347 TLNVND-----PS-----PVPSSSTVHAIIIGGIVAFIVFLLLLMLLFLGHYLI--- 390
Db      331 EVNITEFPYTPPEKRRAGPVT-----AIIGVAGSI-----LVLIVGVGIIVALR 380
Qy      391 --RH--KGYLT-----HEAKGSDDAPDADTAIINAEQSGSG 424
Db      381 RRRHTEKGDYSTKKHVGNGYSKAGIQHPHPMAQNLQYDDSDDEKKA--GPLGGSSE 438
Qy      425 DDKKE 429
Db      439 EEEEE 443

RESULT 11
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <WIL>
A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN000028; CBSP:F15G9.4a
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5175 <W12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN000028; CBSP:F15G9.4a
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: CBSP:F15G9.4a
A:Map position: X
A:Transitions: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1
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Best Local Similarity 24.5%; Pred. No. 1.7e-06;
Matches 80; Conservative 57; Mismatches 124; Indels 66; Gaps 15;
Qy      55 S9PDMLASQDSQWTSDETIV-----VAGGTVLVKQVKDHSDSLQSNPAQQTLYFGE 108
Db      3378 SEQDFKVVYTKFYI-DETIQTPKAVAGEIILKCPVLGNPTPTVWKR-----GD 3428
Qy      109 KRALNDRIQLVTSPTHELISISNVALADEGETCSIFTMPVRTAKSLVTV-----VLGI 163
Db      3429 DAVPNDSRHTIV---NNYDLKINSVTTDEAQYSC---IAVNEAGNLTHVAAEVICK 3480
Qy      164 POKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKTF 223
Db      3481 PTFVRKGNLYEIVENDITWDCGVT-SRPFPISIFWRGDKFVY-LYDRYSISPDG----- 3534

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Db 60 TTERVSQVTWORLD-----GTVV-----AAHPSPGVDFFN----- 90
QY 105 YFGEKRALDRNIQLVSTP-----HELSTISNVALADGEVTCSTFTMPVETAKSLV 158
Db 91 -----SOFKDRLEFVRARPTNADLRATLAFGLRVEDEGNTCFATFNGTRRG-V 144
QY 159 TVLGIPQKP--IITGYKSLREKDTATLNCOSGSKFAARLTWRKQDLHGEPTRIQED 216
Db 145 TMLRVIAOPENHAEAEQVETIGTQSVAVARCVSTGRRPARITW---ISSLGEAKDQEP 201
QY 217 P-NGKTTVSSVTFQVTRDDGASIVCSVNHESLKGADRSSTORIEVLVPTTAMIRPDP 275
Db 202 GIQAGTVIISRYSLVPVGRADGVKVTCTVHEHSEFEE-----PILLFVTLVSRYPP 252
QY 276 PHPREG-----QKLLHCEGRGNPVPQOYLWE-KEGSVPPLKMTQESALIFPLNK 325
Db 253 EVSISGYDDNWLGRSEALITCDVRSNPEPTDWTSTGVPFASAVAQSQQLLVHSDVR 312
QY 326 SDSGTYGCTATNSMGSKAYITLVNNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFL 385
Db 313 MVNTFTICTATNAVGTGRAEQVILVRD---TPQASRDVGLVWGAUGGTLVLLVLAGGFL 369
QY 386 GHYILIRHKGTYLTHEAKSGDDADPADTALINAEGCGSGDDKKEYF 431
Db 370 ALILLRRRRRKSPGGGND-----GDRSGYDPKTVQVF 402

RESULT 7
JC5287
SHP subtrate-1 protein - human
C/Species: Homo sapiens (man)
C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C/Accession: JC5287
R/Yamao, T.; Matozaki, T.; Amano, K.; Matsuoka, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A/Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A/Reference number: JC5287; MUID: 97223399; PMID: 9070220
A/Contents: Brain
A/Accession: JC5287
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-503 <VAM>
A/Cross-references: DDBJ:D86043; MID:g1864010; PID:BAAL2974.1; PID:g1864011
C/Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C/Genetics:
A/Map position: 20p13

Query Match 10.5%; Score 238.5; DB 2; Length 503;
Best Local Similarity 24.2%; Pred. No. 2.3e-09;
Matches 110; Conservative 71; Mismatches 152; Indels 121; Gaps 23;

QY 8 LLLLLLLFACWAPGGANLSQDGWQODLELCTLAPLDEAISSTVWSSPDMLASQDSQP 67
Db 14 LLCLLLAASCANS-----GVAGEELQV--IQP-DKSVS----- 44
QY 68 WTSDETIVAGGTIVLKCQVXKHEDSSL-----QW-----SNPAQOTLYFGEKRALDRNIQ 118
Db 45 -----VAAGESAILHCTV-----TSLIPVGPQIOWFRGAGPARELIY-NQKEGHFPRVIT 92
QY 119 LVSTSTPE---LSSISNVALADGEVTCSTFTMPVETAKSLVTLVGIQKPII 169
Db 93 VSESTKRENMDFSISITNIPADAGTYCYVKFRKGSPTDFKSGAGTSLSVRAKSPAPV 152
QY 170 TGYKSLREKDTATLNCOSGSKPA-ARLTWRKGDOLHGEPTRIQEDNGK--TFTVS 226
Db 153 SGFAARATPHTVSFCESHGFRDITLAKFNKGNELSDQFNV--DPVGEVSYSIHS 210
QY 227 SVTFQVTRDDGASIVCSVNHESLKGAD-RSTSQRIEVLVYPTAMIRPDPHPRREGOKLL 285
Db 211 TAKWLTREDVHSGVCEVAHVTLQDPLRGTLNSETIRVPTLEVTQQPVRAENQ-VN 269
```

```
QY 286 LHCEGRG-NVPPOOYLWEKEGSVPPLKMTQESALIFPLNKSDSGTYGCTATNSMGSYKA 344
Db 270 VTQVCRKFPQRLQLTWLENGV---SRTEASTV---TENKDGTV-----NWMS 313
QY 345 YVTLNV-----NDPSPVPS-----SSSTVHAIIG-----I 370
Db 314 WLLVNVSAHRDDVKLTQCEVHDQPAVSKSHDLKVSAPKPEQGSNTAAENTGSNERNIYI 373
QY 371 VAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGS 404
Db 374 VVGWVCTLLVALLMAALYLVIR-----QKKAQGS 403

RESULT 8
I68093
PRR2 delta - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C/Accession: I68093
R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A/Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A/Reference number: I53960; MUID: 95347610; PMID: 7622062
A/Accession: I68093
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-538 <RES>
A/Cross-references: GB:S79172; NID:g1042204; PID:g1042205
C/Genetics:
A/Gene: PRR2delta
C/Superfamily: poliovirus receptor; immunoglobulin homology
F/276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 225.5; DB 2; Length 538;
Best Local Similarity 23.9%; Pred. No. 2.1e-08;
Matches 82; Conservative 52; Mismatches 146; Indels 63; Gaps 13;

QY 77 GGTVLKCOV-----KQED-----SSLOSNPAQOTLYF- 106
Db 47 GGTVELPCHLLPVPGLYISLTWQRPDAPANHQVAAFHPKMGSPFPSPKGSERLSFV 106
QY 107 -GEKRALDRNIQLVSTSTHELSTISNVALADGEVTCSTFTMPVETAKSLVTLVGIQ 165
Db 107 SAKQSTGQTEAELODAT-----LALHGLTVEDEGNTCEFATFPKSGVRGM-TWLRVIA 160
QY 166 KP--IITGYKSLREKDTATLNCOSGSKPAARLTWRKGDOLHGEPTRIQEDPNKTT 223
Db 161 KPNQQAQKVTFSSQDPTTVALCISKEGPPARISW-LSSLDWEAKETQVSGTLG-TVT 218
QY 224 VSSSVTFQVTRDDGASIVCSVNHESLKGADRSSTORIEVLVPTTAMI-----RP 273
Db 219 VTSRFTLVPSGRADGVTVTKVHEHSFE-EPALIPVTLVSRVPEVVISGYDDNWYLGRT 277
QY 274 DPHPREGOKLLHCEGRGNPVPQOYLWE-KEGSVPPLKMTQESALIFPLNKSDSGTYG 332
Db 278 D-----ATLSCDVRNPEPTGYDWTSTGTSPTSAVAGSQSLVIAHVDLSLFTTFV 328
QY 333 CTATNSMGSKAYITLVNNDPSPVPSSSTYHAIIGGIVAFIV 375
Db 329 CVTVNAVGMGRAEQVIFVRE--TPNTAGAGATGGTIGGIIAAII 370

RESULT 9
JC5519
50K Glycoprotein precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
C/Accession: JC5519
R/Hancock, K.A.; Gooley, A.A.; Jeffrey, P.L.
Mol. Brain Res. 44, 273-285, 1997
A/Title: AvG500, a predominantly axonally expressed glycoprotein, is a member of the Igi
A/Reference number: JC5519; MUID: 97225899; PMID: 9073169
A/Accession: JC5519
```

A:Molecule type: mRNA
A:Residues: 1-66, A', 68-417 <MEN>
A:CROSS-references: GB:M29535
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C:Genetics:
A:Gene: GDB:PVR; PVS
A:CROSS-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F:21-343/Domain: extracellular #status predicted <EXT>
F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F:42-125/Domain: immunoglobulin homology <IMW1>
F:159-223/Domain: immunoglobulin homology <IMW2>
F:259-314/Domain: immunoglobulin homology <IMW3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 11.7%; Score 265; DB 1; Length 417;
Best Local Similarity 26.6%; Pred. No. 2.4e-11;
Matches 106; Conservative 59; Mismatches 173; Indels 62; Gaps 17;

QY 5 AASLLLLLLFACCAWPGGANLSQDGYWQEDLELTP--LDEAISSTVW--SSDMLA 61
DB 7 AAWPLLLVALLVSWPPPGTG-----DVVQAPQTQVPGFGDSVTPLCYLQVPMNEV 58
QY 62 SQDSQ--PWSDETVVAGTVVLKQVKDHEDSSLOWNSPAQOTLYFGKEKRALRDNRILQV 120
DB 59 THVSQLTWT-----RHGSGSMVAFHQTQGPSYSEK-----RLEFV 95
QY 121 TSPHELSSISNVAL-----ADSGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITG-- 171
DB 96 AA-----FLGELRNASLUMFGLRVEDSGNTCLFVTFP--QGSRSVDIWLRLAKPQNTAEV 151
QY 172 YKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPN--GKFTVSSSVT 229
DB 152 QKVLTGEPVPMARCVSTGRRPPAQITWH---SDLGMPNTSQV--PGFLSGTIVTISLMT 207
QY 230 FQWTRDDGASIVCSVNHSLKAGDRSTQRIEVLVTPMTIRPDPPHREGO--KLLHLC 288
DB 208 LVPSSQVDGKNTCKVEHSEFEPKQLLT--VNLTVYYPPEVSGYDNNWYLGQNEATLTC 266
QY 289 EGRGNVPQOYLWEKE--GSVPPPLKMTQESALIPFLNKSQDGYGCTATSNMGSKYAYT 347
DB 267 DARSNPEPTGYNWSVTMGPLPFAVAQAGQLLRPVDPKPIINTLNCVNLGARGAQLT 326
QY 348 LNVNDSPVSSSTVHAIGGIVAFIVFLLLMFLFLG 386
DB 327 VQVKEGPPSEHSGMSRNAII-----FLVLGILVFLILG 360

RESULT 5
AS3437
poliovirus receptor mpvr - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
A:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with p
A:Reference number: A53437; MUID:94179228; PMID:8132569
A:Accession: A53437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <AOK>
A:CROSS-references: GB:D26107; NID:9475017; PIDN:BAA05103.1; PID:9825507
A:Experimental source: C57/Bl6, brain
A>Note: sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)

C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMW>
Query Match 11.3%; Score 256; DB 2; Length 530;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
Matches 100; Conservative 52; Mismatches 160; Indels 98; Gaps 16;

QY 3 APAASLLLLLLFACCAWPGGANLSQDGYWQEDLEL-----GT-----LAP 44
DB 13 SPTPLPLPLLLL-----LQETG---AQDVRVRLPEVRGLGGTVLPLCHLLPP 59
QY 45 LDEAISSTVSSPDMLASQDSQFWTSDETVAAGTVVLKQVKDHEDSSLOWNSPAQOTL 104
DB 60 TTERVSVQVWORLD-----GTVV-----AAHPSFGVDFPN----- 90
QY 105 YGKERALRDNRILQVTSPT-----HELSISNVALADEGEYTCSTFTMPVTRAKSLV 158
DB 91 -----SQFSKDRLSFVRARPETNADLRDATLAFRLGRVDEGNYTCEFATFNGTRRG-V 144
QY 159 TVLGIPOKPE--IITGYKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQED 216
DB 145 TWLRLVIAQEPENAEAEQEVITIGQSVAVARCVSTGRRPPARIW---ISSLGKAKDTQBP 201
QY 217 P--NGKFTVSSSVTQVTRDDGASIVCSVNHSLKAGDRSTQRIEVLVTPMTIRPD 275
DB 202 GIQAGTVTIIISRYSLVPVGRADGVKVTCTVHEHSEFEE-----PILLPVLSVRYEP 252
QY 276 PHREG-----QKLLHCEGRNVPVPOQYLWE--KEGSPVPLKMTQESALIFPFLNK 325
DB 253 EVSISGYDDNWLGRSEAILTCDVRSNPEPTDYDWSITSGVFPASAVAQGSQLLVHSVDR 312
QY 326 SDSGTVGCTATSNMGSKYAYTLNVNDSPVSSSTVHAIGGIVAFIV 375
DB 313 MUNTFFICTATNAVGTGRABQVILVRE--SPSTAGAGATGGIIGGIIAII 361

RESULT 6
HLMSP3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
A:Accession: A38211
R:Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:CROSS-references: GB:M80206; NID:919785; PIDN:AAA39734.1; PID:9199786
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <EXT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homology <IMW1>
F:167-231/Domain: immunoglobulin homology <IMW2>
F:267-322/Domain: immunoglobulin homology <IMW3>
F:355-374/Domain: transmembrane #status predicted <TMN>
F:375-467/Domain: intracellular #status predicted <INT>
F:54-131,174-229,274-320/Disulfide bonds: #status predicted
F:128,136,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 254.5; DB 1; Length 467;
Best Local Similarity 23.2%; Pred. No. 1.5e-10;
Matches 108; Conservative 59; Mismatches 186; Indels 113; Gaps 17;

QY 3 APAASLLLLLLFACCAWPGGANLSQDGYWQEDLEL-----GT-----LAP 44
DB 13 SPTPLPLPLLLL-----LQETG---AQDVRVRLPEVRGLGGTVLPLCHLLPP 59
QY 45 LDEAISSTVSSPDMLASQDSQFWTSDETVAAGTVVLKQVKDHEDSSLOWNSPAQOTL 104

A;Gene: GDB:PVR; PVS

A;Cross-references: GDB:120324; OMIM:173850

A;Map position: 19q13.2-19q13.2

A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1

C;Superfamily: poliovirus receptor; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-392/Product: poliovirus receptor delta #status predicted <MAT>

F;21-343/Domain: extracellular #status predicted <EXT>

F;42-125/Domain: immunoglobulin homology <IMM1>

F;159-223/Domain: immunoglobulin homology <UMM2>

F;259-314/Domain: immunoglobulin homology <IMM3>

F;344-367/Domain: transmembrane #status predicted <TMN>

F;368-392/Domain: intracellular #status predicted <INT>

F;49-123,166-221,266-312/Disulfide bonds: #status predicted

F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 11.7%; Score 265; DB 1; Length 392;
Best Local Similarity 26.6%; Pred. No. 2,2e+11;
Matches 106; Conservative 58; Mismatches 173; Indels 62; Gaps 17;

QY 5 AASLLLLLLFACCAWPGGANLSQDGYWQBDELGLAP--LDEAISSTVW--SSPDMLA 61
||| ||| : : : : : : : : : : : : : : : : :
Db 7 AAWEPLLIALLVLNSWPPGPGT-----DVVVQAPTQVEGFLGDSVTLPCLQVPNMEV 58
||| ||| : : : : : : : : : : : : : : : : :
QY 62 SQDSQ--PWISDETIVAGGTIVLKCVKQKHEDSSLWSNPAAQTLYEGEGRALDRNIQLV 120
||| ||| : : : : : : : : : : : : : : : : :
Db 59 THVSQITWT-----RHGESGMAYFHQTQGPSYSESK-----RLEEV 95
||| ||| : : : : : : : : : : : : : : : : :
QY 121 TSTPHELISISINVAL-----ADEGETCTGFTMPVRTAKSLVTLVGIPQKIITG-- 171
||| ||| : : : : : : : : : : : : : : : : :
Db 96 AA---RLGAELRNASLMFGLRVDESGNTCLFVTFP-QGSRSVDILWLAKPONTAEV 151
||| ||| : : : : : : : : : : : : : : : : :
QY 172 YKSLEKEKTATLNCOSSSKPAARLTWRKGQDLHGEFTRIQEDN--GKTFVTSSSVT 229
||| ||| : : : : : : : : : : : : : : : : :
Db 152 QKVOLTAGEPVPMARCVCSTGCRPPAQITWH---SDLGCMNTSQV-PGFLSGTVTTSLMI 207
||| ||| : : : : : : : : : : : : : : : : :
QY 230 FQVTRDDGASIVCSVNHSLSKADRSTQRTELVYTPAMIRPDPPHREG-KLLHLHC 288
||| ||| : : : : : : : : : : : : : : : : :
Db 208 LVPESSQVDGNVTKVEHSEFEKPQLLT-VNLTVTYPPPEVSGVDNNWYLQNENALTLC 266
||| ||| : : : : : : : : : : : : : : : : :
QY 289 EGRGNVPQQYLWEKE-GVPPVKMTQESALIFPFPLINKSDSCTYGCTATSNMGSYKAYYT 347
||| ||| : : : : : : : : : : : : : : : : :
Db 267 DARSNEPTGYNMSTMTPGLPFFFAVAQGALLRPVDKPIPTTLLICNVTNALGARQEAELT 326
||| ||| : : : : : : : : : : : : : : : : :
QY 348 LNVNDPSVPSSSTVHAIIIGGVAFIVFILLIIMLIFLG 386
||| ||| : : : : : : : : : : : : : : : : :
Db 327 VQVKEGPPEHSGMSRNAI-----FLVLGIIVFLILLG 360
||| ||| : : : : : : : : : : : : : : : : :

RESULT 4

RWHUPA

N;poliovirus receptor splice form alpha precursor - human

N;Alternate names: poliovirus receptor H20A

N;Contains: poliovirus receptor beta

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text change 22-Jun-1999

C;Accession: S12048; A31496

R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Izuka, N.; Takeuchi, K.; Takeuchi, K.; Takeuchi, K.

EMBO J. 9, 3217-3224, 1990

A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted forms.

A;Reference number: S12048; PMID:91006015; PMID:2170108

A;Accession: S12048

A;Molecule type: DNA

A;Residues: 1-417 <KOI>

A;Cross-references: EMBL:X64116; NID:g35809; PIDN:CAA45478.1; PID:g825708

A;Note: 67-Ala was also found

A;Note: The gamma form has 331-Gly and lacks residues 332-384

R;Wendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989

A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and characterization of the receptor protein.

A;Reference number: A90910; PMID:89168426; PMID:2538245

A;Accession: A31496

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.4885 Seconds
(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPAAALLLLLLLAFACWA.....AIINAEQGSGDDKXEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	12.0	417	2 A44194	poliovirus recepto
2	270.5	11.9	392	2 B44194	poliovirus recepto
3	265	11.7	392	1 RWHUPD	poliovirus recepto
4	265	11.7	417	1 RWHUPA	poliovirus recepto
5	256	11.3	530	2 A53437	poliovirus recepto
6	254.5	11.2	467	1 HLMSF3	poliovirus recepto
7	238.5	10.5	503	2 JCS287	SHP substrate-1 pr
8	225.5	10.0	538	2 I68093	PRR2 delta - human
9	223	9.8	338	2 JCS519	50K glycoprotein p
10	221.5	9.8	518	2 JC4024	poliovirus recepto
11	217	9.6	5175	2 T20992	hypothetical prote
12	217	9.6	5198	2 T43290	hemocentin precurs
13	216.5	9.6	702	2 A36319	carcinoembryonic a
14	215	9.5	739	2 JS0675	vascular cell adhe
15	213.5	9.4	478	2 I53960	PRR2 alpha - human
16	212.5	9.4	583	2 I39428	alcam - human
17	209	9.2	4391	2 A38096	perlecan precursor
18	208	9.2	338	2 JCI238	opioid-binding pro
19	208	9.2	345	2 JCI239	opioid-binding pro
20	208	9.2	1612	2 T30805	dutt1 protein - mo
21	207	9.1	345	2 JC4025	opioid-binding cel
22	207	9.1	7962	2 I38346	elastic tctin - hu
23	205	9.1	338	2 JC4776	limbic-system-asso
24	204	9.0	509	2 JCS288	SHP substrate-1 pr
25	204	9.0	513	2 JCS289	SHP substrate-1 pr
26	203	9.0	345	2 S03199	opioid-binding pro
27	202	8.9	1651	2 T14160	transmembrane rece
28	197.5	8.7	547	1 S28904	intercellular adhe
29	196	8.7	344	2 I56551	neurotrimin - rat

30 196 8.7 3707 2 S18252 heparan sulfate pr
31 194 8.6 1427 2 I51669 tumor suppressor -
32 192.5 8.5 1051 2 A39712 kinase-like protei
33 191.5 8.5 1443 2 I50600 neogenin - chicken
34 191 8.4 764 2 A49448 irregular chiasm C
35 189 8.3 407 2 T08732 hypothetical prote
36 188 8.3 3375 2 T19821 hypothetical prote
37 187.5 8.3 523 2 I50478 neurotin - goldfis
38 187.5 8.3 588 2 JH0506 adhesion molecule
39 187.5 8.3 588 2 A45254 surface glycoprote
40 187.5 8.3 4162 2 T42633 connectin/titin -
41 186.5 8.2 1273 2 T42405 sax-3 protein - Ca
42 184 8.1 402 2 T09062 probable advanced
43 183.5 8.1 416 2 A54017 colon carcinoma-as
44 182.5 8.1 628 2 I38000 lutheran blood gro
45 180.5 8.0 1011 2 T13669 neuromusculin - fr

ALIGNMENTS

RESULT 1
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: A44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no put
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: A44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-417 <XOI>
A/Cross-references: GB:S48777
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 12.0%; Score 272; DB 2; Length 417;
Best Local Similarity 26.2%; Pred. No. 7.5e-12;
Matches 106; Conservative 56; Mismatches 183; Indels 60; Gaps 16;

QY 67 PWTSDTVA-----GGTVLKC--QVKHED---SSLQSNPAQ-----QT 103
Db 24 PGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSLQTSRHSQSGSMAVPHQTQ 83
QY 104 LYFGEKRALRDNRQLQVTSHPHELSISISNALADGEYTCSTFTMPVRTAKSLVTVLGI 163
Db 84 PNYSEPKRLEFVAARLGTGL-RLDALRMFGLRVEDGNTCLFVTTP-QGSRSDIWLRL 141
QY 164 PKPITG--YKSLREKDTATINCQSSGSKPAARLTWRKQDLHGEPTRIQEDEN--G 219
Db 142 LAKPQNTAEVQVQLTGKVPVAVRCVSTGGRPPAHTWH---SDLGMENTQA-PGFLS 197
QY 220 KFTFTSSSVTFQVTRDDGASIVCSVNHELKAGDRSTQRIEVLVYPTFAMIRP-DPPHP 278
Db 198 GVTVTSLWILVPSSQVDGKSVTCVHEHSEPKQLLT-VNLTVVYPPEVSIQYDNNWY 256
QY 279 REGQKLLHCEGRGNVPVQOYLWEKE-GSVPLKMTQESALIFPFINKSDSTYGTGTS 337
Db 257 LSONEATITCDARSNPETGYNNSTMTGPLPFPAVQAQQLIRVPDPIKNTFTTCVNTN 316
QY 338 NMGYSKAYTYLNVND-PSFPVSSSTYHAIIGGIVAFIVFLLILMLIFLG----- 386
Db 317 ALGAQAELTVQVKEGPPSEFGMS-----NIIFLLIGVILLTLGLGIVYRRC 370
QY 387 -----HYLRHKGTYYLTHAKGSDDDAPDADTAIINAEQSGG 424
Db 371 SREFLWCHHLSFSEHASAGANGYISYDVSREASSQDDPQTEG 415


```

Db      69  TLTFGEKRALDRNRIQLVTSTPHELSISISNALADEGEYTCISFTMPVTRAKSLVTLVG 128
      125  PPRNLMIIDIKDXTAVEGEIEVNCMTAKSGPATIRWFKGNKELGK-SEVEEWS-D--MY 181
Db      129  IQPKFIITGYKSSUREKDTATLNCQSGSGPAARLTKRKGDELHGEPTRIQBDPNGKTF 188
      182  TVTSQMLMKVHKEDDGVFVICQVEHPAVTG-NIQTORYLEVQYKPVQVHIQMTYPLQGLTR 240
Db      189  TVSSSVTFQVTRDDGASIVCSVNHESLKADRSISQRIEVLVYTPAMIRPDP--HFR 245
      241  EGDABELCEAIGKQPQVMTWVRVDDMPQHAVLGGPNLFINNKNKTONGTYRCEASNI 300
Db      246  EGQKLLHCEGRGNVPVQOYLWEK-EGSVPLKMTQBSALIFPLFNKSDSGTYGCTATSN 304
      301  VGKASHDVMLYVYDPPPTPIPPPTTTTTTTTTTTTTTTTTITLITDSRAGEEGTIGAVDHAVIG 360
Db      305  MGSYKAYTLNVNDES---VPSSSTY-----HAIG 334
      361  GVVAVVVFAMLCILIIIGRYFARHKGYTFTHKAGDADAADATAIINAEQGNNEEEK 420
Db      335  GIVATVFLMLIMLIFLGHYLLRHKGTYLTHKAGSDADPADATAIINAEQSGSGDDKK 394
      421  EYF 423
Db      395  EYF 397

RESULT 14
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match 32.6%; Score 715.5; DB 4; Length 432;
Best Local Similarity 36.1%; Pred No. 2.4e-55;
Matches 165; Conservative 75; Mismatches 140; Indels 77; Gaps 10

      QY 10 LLLLLLAAALIPTG-----DG-----QNL-----F 30
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      Db 9 LLLLLLACCWAPGAGNLSDQGYWQEDLEGLTAPLDEALISSTWSSPDLASQDSQPW 68
      QY 31 TKDVTVIEGEVATISCVNKSDDSVTLQLNPNRQTYTFRDFPLKDRPQLNPFSSSELK 90
      Db 69 TSDETWAGGTWVLKCKQKHEDSSLOWSNPAQCTLYFGEKRALDRNRIQLVTSTPHELS 128
      QY 91 VSLTNVISDSDEGRYFCOLYTDPPQESVTTITVLVPPRNLMIIDIKDXTAVEGEIEVNC 150
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      Db 129 ISISNALADEGEYTCISFTMPVTRAKSLVTLGIPQKPIITGYKSSUREKDTATLNCQ 188
      QY 151 MASKEPATIRWFKGNKELGK-SEVEEWS-D--MYTVTSQMLMKVHKEDDGVFVICQVEHP 207
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      Db 189 SGSKEPAARLTKRKGDELHGEPTRIQBDPNGKTFTVSSSVTFQVTRDDGASIVCSVNH 248
      QY 208 AVTG-NIQTORYLEVQYKPVQVHIQMTYPLQGLTREGDAFELTCEAIGKQPQVMTWVRV 266
         ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 249 SLKGADRSISQRIEVLVYTPAMIRPDP---HPREGKLLHCEGRGNVPVQOYLWEK-E 304

```


Db 363 VVFVTLCSIFLLGRYLARHKGYLTNEAKGADAPDADTAIINAEAGSQVNAEKKKEYF 420

RESULT 8
US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-660-531-1

Query Match 40.7%; Score 893.5; DB 3; Length 421;
Best Local Similarity 45.0%; Pred. No. 3.3e-71;
Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;
QY 26 GQNLFTKDVTVIEGEVATISQVKNKSDSVIQLNPNRQTIYFRDPRPLKDSRFOLLNFS 85
Db 10 GGFPLTQNVTVVEGGTAITLCTDQNDNTSLQSNPAQQTLYFDKALRDRNRIELVRAS 69
QY 86 SSELKSLTNVSDSGRYFCOLYTDPPQESYTTITVLVPPNLMIDIQKQAVGEIE 145
Db 70 WHELISVSDVSLDEGGQTCSLFTMPVKTSKAYLTVLGVPKEPKQISGFSSPVMGDLMQ 129
QY 146 VNCTAMASKPATIRFWKGNKELKGKSEVEWS---DMYTVTSQMLKVKHEDDGVFVIC 202
Db 130 LTKCTSGSKFAADIRWFKNDKEIKDKVEDANRKTFTVSTLDFRVDSDGAVIC 189
QY 203 QVEHPAVTGNLQ--TORYLEVQKPKQVHIOMTYPLQGLTREGDAFELTCEAIGKPPQVMVT 261
Db 190 RVDHESINATPQVAMQVLEIHYTPSVKI---IPSTFPQEGQPLILTCESKGKPLPEPUL 246
QY 262 WVRVDDEM--PQHAVLSGPNLFINNKNKTNGTYRCEASNIVGKAHSDYMLYVYDPPPTI 319
Db 247 WTKDGGELPDDRWVWVGRELNLFNKNKTNGTYRCEATNTIGSSABYVLIVHDVNTL 306

QY 320 PPPTTTTTTTTTTTTTTTTTIT-----DSRAGEBTIGAVDHAIVGGVAV 365
Db 307 LPTTIIPSLTATVTTTVAITTSPTTSATTSIRDPNALAGNGP----DHALIGGI VAV 362
QY 366 VVFAMCLLIILGRYFAHKGTYTHEAKGADDAADADTAIINAEAGSQVNAEKKKEYF 423
Db 363 VVFVTLCSIFLLGRYLARHKGYLTNEAKGADAPDADTAIINAEAGSQVNAEKKKEYF 420

RESULT 9
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B711
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PPT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 33.6%; Score 738.5; DB 4; Length 398;
Best Local Similarity 38.8%; Pred. No. 1.9e-57;
Matches 165; Conservative 73; Mismatches 136; Indels 51; Gaps 9;
QY 12 LLLLSAAALIPTG-----DQNLFTKDVTVIEGEVATISQVKNKSDSVIQLNPNRQTI 66
Db 11 LLLLLACSWAPGGANLSQDSSQPTSDVTVAGTVLKCQVKDHDSSLQWNSNPAQQT 70
QY 67 YFRDPRPLKDSRFOLLNFSSELKSLTNVSDSGRYFCOLYTDPPQESYTTITVLVPP 126
Db 71 YFGEKRALRDRNRIOLVSTPHELSISINVALADEGEYTCSTFTMPVTKSLVTVLGP 130
QY 127 RNLMDIQKDTAVEGEEIEVNCWTAMASKPATIRFWKGNKELKG--KSEVEWSD--MYTV 183
Db 131 QKPIITGYKSSLREKETATLNCQSSGSKPAAOLTWRKQDQLHGDQTRI QEDPNKGTFTV 190
QY 184 TSQMLKVKHEDDGVFVICQVEHPAVTG--NLQORYLEVQYKPKQVHIOMTYPLQGLTREG 242
Db 191 SSSVSFQVTRDGDGANIVCSVNHESLKGADRTSQRILEVLYTPTAMIR---PEPAHPREG 247
QY 243 DAFELTCEAIGKPPQVMVTWVRVDDEM-----QHAVLSGPNLFINNKNKTNGTYRCEAS 298
Db 243 QKLLHCSGRGNPVPQQYVWVKEGSEPELKMVQESALIFP-----FLNKSDSGTYGCTAT 302
QY 299 NIVGKAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTITITDTSRAGEBTIGAVDHA 358
Db 303 SNMGSYTAFTLVNDPS---PVSSSSSTY-----HAI 332
QY 359 IGVVAVVVFAMCLLIILGRYFAHKGTYTHEAKGADDAADADTAIINAEAGSQVNAEKKKEYF 418
Db 333 IGGIVAFIVFVLLILLIFLGHYLRHKGYLTNEAKGADAPDADTAIINAEAGSQVNAEKKKEYF 392
QY 419 KKEYF 423
Db 393 KKEYF 397

RESULT 10
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:

; Sequence 1, Application US/08659984A

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match
Best Local Similarity 97.8%; Score 2149; DB 4; Length 440;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPPGLRLRLLLLSAALPTGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 AAPPG--LRLLLLLSAALPTGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 76
QY 61 PNRQTIYPRDPRPLKDSRFQLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
77 PNRQTIYPRDPRPLKDSRFQLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 136
QY 121 TVLPPRNLMDIOKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 TVLPPRNLMDIOKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 196
QY 181 YTVTSQLMLKVHKEDDGPVPCQVEHPAVTGNLQTVLEVQYKQVHIQMTYPLQGLTR 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
197 YTVTSQLMLKVHKEDDGPVPCQVEHPAVTGNLQTVLEVQYKQVHIQMTYPLQGLTR 256
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGNFLINNLTNDNGTYRCEASNI 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
257 EGDALFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGNFLINNLTNDNGTYRCEASNI 316
QY 301 VGKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
317 VGKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
QY 361 GVAVVVFAMLCLLIILGRYFARHKGYFTHEAKGADDAADATTAIINAGGQNNSEKK 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
377 GVAVVVFAMLCLLIILGRYFARHKGYFTHEAKGADDAADATTAIINAGGQNNSEKK 436
QY 421 EYF 423
Db |||||
437 EYF 439

RESULT 5
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-5

Query Match
Best Local Similarity 41.1%; Score 904; DB 2; Length 444;
Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;

QY 13 LLISAAA---LIPTGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLNPRQTIYFR 69
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
77 LLQAAAKNKVKSGQGFPLTQNTVVEGGTALTTCRVQNDNTSLQWSNPAQQTLYFD 76
QY 70 DERPLKDSRFQLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTITVLVPPRNL 129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
77 DKALRDNRLELVRASWHELISISVDSVLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKP 136
QY 130 MIDIQDQDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEWS--DMYTVTSQ 186
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 QISGFSPPVMEGLMQLTCKTSGSKPAADIRWFKNDKEIKDVYLKEEDANRKTFTVSST 196
QY 187 LMLKVHKEDDGPVPCQVEHPAVTGNLQ--TVLEVQYKQVHIQMTYPLQGLTREGDAF 245
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 LDFRVDRSDGGAIVCRVDHESLNATPQAMQVLEIHYTPSVKI---IPSTPPFQEQPL 253
QY 246 ELTCEAIGKQPQVMTWVRVDDMP--PQHAVLSGNFLINNLTNDNGTYRCEASNI 303
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
254 ILTCESKGKFLPEPLVLTQGGELPDPDRWVSGREINILFNKNTDNGTYRCEATNTIGQ 313
QY 304 AHSYDMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
314 SSAEYVLIVHDVENTLLPTTIIPSLTATVTTVAITTSPTTSATTSIRDPNALAGQNG 373
QY 350 TIGAVDHAIVGGVAVVVFAMLCLLIILGRYFARHKGYFTHEAKGADDAADATTAIINA 409
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 P----DHALIGGIVAVVVFVETICSLIFLLGRYLARHKGYTLTNEAKGADAPADATTAIINA 429
QY 410 EGGQNNSEKKEYF 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
430 EGSQVNAEKEYF 443

RESULT 6
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
```


QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 420
Db |||||
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 420
Db |||||
QY 421 EYF 423
Db |||||
QY 421 EYF 423

RESULT 2

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095

GENERAL INFORMATION:

; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-778-510-20

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
Db 79 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPPRNLMDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPRNLMDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPOPMVMTVRVDDMPQHAVLSPGNLFNNLNKTDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPOPMVMTVRVDDMPQHAVLSPGNLFNNLNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTTPPTTT 360
Db 319 VGKASDYMLYVYDPTTTPPTTT 378
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 420
Db 379 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 3

US-09-930-803-1

; Sequence 1, Application US/09930803

; Patent No. 6596493

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPPGLRLRLLLLSAAALIPGDCGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
Db 79 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPPRNLMDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPRNLMDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPOPMVMTVRVDDMPQHAVLSPGNLFNNLNKTDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPOPMVMTVRVDDMPQHAVLSPGNLFNNLNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTTPPTTT 360
Db 319 VGKASDYMLYVYDPTTTPPTTT 378
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 420
Db 379 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADADATTAIINAEAGGONNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 4

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 15.4726 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLLLLLSAAAL.....TAINAEGQNNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*

3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*

4: /cgn2_6/prodata/2/iaa/6B COMB.pcp.*

5: /cgn2_6/prodata/2/iaa/6C COMB.pcp.*

6: /cgn2_6/prodata/2/iaa/6D COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2169	98.7	442	4	US-09-778-510-20
3	2169	98.7	442	4	US-09-930-803-1
4	2149	97.8	440	4	US-09-866-028-61
5	904	41.1	444	2	US-08-659-984A-5
6	904	41.1	444	3	US-08-660-531-5
7	893.5	40.7	421	2	US-08-659-984A-1
8	893.5	40.7	421	3	US-08-660-531-1
9	738.5	33.6	398	4	US-09-778-510-4
10	732.5	33.3	398	4	US-09-907-794A-84
11	732.5	33.3	398	4	US-09-778-510-6
12	732.5	33.3	398	4	US-09-905-125A-84
13	732.5	33.3	398	4	US-09-902-775A-84
14	715.5	32.6	432	4	US-09-778-510-2
15	333	15.2	227	4	US-09-205-258-947
16	252.5	11.5	517	4	US-09-723-368-4
17	244	11.1	518	4	US-09-919-172-20
18	231.5	10.3	393	1	US-08-429-742-2
19	226.5	10.3	479	4	US-09-723-368-2
20	220.5	10.0	344	4	US-09-700-397-3
21	216	9.8	458	4	US-09-435-956A-1
22	212	9.6	313	4	US-09-700-397-4
23	206.5	9.4	308	2	US-08-414-657D-46
24	206.5	9.4	325	2	US-08-414-657D-2
25	206.5	9.4	325	2	US-08-414-657D-41
26	206.5	9.4	325	4	US-09-135-080-2
27	206.5	9.4	338	4	US-09-976-594-404

28	206	9.4	388	1	US-08-429-742-4	Sequence 4, Appli
29	205.5	9.4	582	4	US-09-702-705-334	Sequence 334, App
30	205.5	9.4	582	4	US-09-736-457-334	Sequence 334, App
31	205.5	9.4	582	4	US-09-614-124B-334	Sequence 334, App
32	205.5	9.4	582	4	US-09-671-325-334	Sequence 334, App
33	205.5	9.4	582	4	US-09-589-184-334	Sequence 334, App
34	204.5	9.3	315	2	US-08-414-657D-47	Sequence 47, Appl
35	204.5	9.3	338	2	US-08-414-657D-42	Sequence 42, Appl
36	204.5	9.3	338	4	US-09-135-080-4	Sequence 4, Appli
37	204.5	9.3	642	1	US-08-217-299-1	Sequence 1, Appli
38	204	9.3	698	2	US-08-602-725-36	Sequence 36, Appl
39	204	9.3	734	4	US-08-389-459A-17	Sequence 17, Appl
40	204	9.3	734	3	US-08-987-867A-17	Sequence 17, Appl
41	204	9.3	734	2	US-08-432-016-2	Sequence 2, Appli
42	203.5	9.3	583	2	US-08-684-594-2	Sequence 531, App
43	203.5	9.3	583	2	US-08-414-657D-60	Sequence 60, Appl
44	203	9.2	1461	4	US-09-976-594-531	
45	198.5	9.0	338	2	US-08-414-657D-60	

ALIGNMENTS

RESULT 1

US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated BYL1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match	100.0%	Score	2197	DB	4	Length	423
Best Local Similarity	100.0%	Pred. No.	3.6e-187	Mismatches	0	Indels	0
Matches	423	Conservative	0	Mismatches	0	Gaps	0
OY	1	AAPPGLRLRLLLLLSAAALIFTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN	60				
DB	1	AAPPGLRLRLLLLLSAAALIFTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN	60				
OY	61	PNRQTIYFRDFRPLKDSRFQNLNFSSSELKSLTVNVSISDEGRYFCQLYTDPQBSYTTI	120				
DB	61	PNRQTIYFRDFRPLKDSRFQNLNFSSSELKSLTVNVSISDEGRYFCQLYTDPQBSYTTI	120				
OY	121	TVLVPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATIRFWKGNKELKGKSEVEWSDM	180				
DB	121	TVLVPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATIRFWKGNKELKGKSEVEWSDM	180				
OY	181	YTVTSQLMKVHKHEDDGVPIVCQVEHPAVTGNLTQRYLVEQYKPVHIOQTYPLQGLTR	240				
DB	181	YTVTSQLMKVHKHEDDGVPIVCQVEHPAVTGNLTQRYLVEQYKPVHIOQTYPLQGLTR	240				
OY	241	EGDAFELTCEAIGKQPQPMVTWVVDDEMPQHAVLSGNLFINLNKTDNCTYRCEASNI	300				
DB	241	EGDAFELTCEAIGKQPQPMVTWVVDDEMPQHAVLSGNLFINLNKTDNCTYRCEASNI	300				
OY	301	VGAHSDYMLVYDPEPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	360				
DB	301	VGAHSDYMLVYDPEPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	360				

Db 377 GVAVVVFAMLCLLIILGRYFARHKGTFTHEAKGADDAADADTAIINAEGQNNSEKK 436
Qy 421 EYF 423
Db 437 EYF 439

Search completed: May 27, 2004, 09:31:23
Job time : 49.4142 secs

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QY 181 YTVTSQMLKVHKEDDGVPIVCQVEHPAVTGNLTQRYLEVQYKQVHVH QMTYPLQGLTR 240
Db 197 YTVTSQMLKVHKEDDGVPIVCQVEHPAVTGNLTQRYLEVQYKQVHVH QMTYPLQGLTR 256
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
Db 257 EGDALFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 316
QY 301 VGKAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 317 VGKAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
QY 361 GWAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 420
Db 377 GWAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 436
QY 421 EYF 423
Db 437 EYF 439

RESULT 15
AAB01321
ID AAB01321 standard; protein; 440 AA.
XX
AC AAB01321;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human PRO355 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
KW PRO715; PRO241; PRO323; PRO299; PRO344; PRO347; PRO355; PRO353;
KW PRO361; PRO365; transmembrane polypeptide; antibody; screening;
KW detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT 1. .36 Location/Qualifiers
FT /label= Signal peptide
FT /note= "N-myristoylation site"
FT /note= 65. .69
FT Modified-site
FT /note= 99. .103
FT Modified-site
FT /note= 111. .115
FT Modified-site
FT /note= 163. .167
FT Modified-site
FT /note= 227. .233
FT Modified-site
FT /note= 233. .240
FT Modified-site
FT /note= 302. .306
FT Modified-site
FT /note= 306. .310
FT Modified-site
FT /note= 307. .313
FT Modified-site
FT /note= 319. .328
FT Modified-site
FT /note= 365. .371
FT Modified-site
FT /note= 372. .393
FT Domain
FT /label= Transmembrane domain
FT /note= 376. .382
FT Modified-site
FT /note= 402. .408
FT Modified-site
FT /note= 411. .417
FT Modified-site
FT /note= "N-myristoylation site"

```

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FT Modified-site 427. .433
FT /note= "N-myristoylation site"
FT Modified-site 428. .432
FT /note= "N-myristoylation site"
FT Modified-site 430. .434
FT /note= "N-glycosylation site"
XX
FN WO200032776-A2.
XX
PD 08-JUN-2000.
XX
PF 01-DEC-1999; 99WO-USQ28301.
XX
PR 01-DEC-1998; 98WO-USQ25108.
XX
PR 16-DEC-1998; 98US-0112850P.
XX
PR 22-DEC-1998; 98US-0113296P.
XX
FA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kljavin IU, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2000-412324/35.
DR N-PSDB; AAA49563.
XX
PT New human nucleic acids encoding secreted and transmembrane polypeptides,
PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PT agents.
XX
PS Claim 12; Fig 24; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane polypeptides
CC which are designated as PRO polypeptides are described The membrane-bound
CC proteins have various industrial applications, including as
CC pharmaceutical and diagnostic agents. The membrane-bound proteins can
CC also be employed for screening of potential peptide or small molecule
CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO
CC antibodies are useful for the affinity purification of PRO from
CC recombinant cell culture or natural sources
XX
SQ Sequence 440 AA;

Query Match 97.8%; Score 2149; DB 3; Length 440;
Best Local Similarity 98.3%; Pred No. 5.8e-148;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPGRLRLRLLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLN 60
Db 19 AAPPG--LRLLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLN 76
QY 61 PNQTIYFRDPRFLKDSRFQNLNFSSELKYSLTNVSISDEGRYFCQLYTPDPQSYTTI 120
Db 77 PNQTIYFRDPRFLKDSRFQNLNFSSELKYSLTNVSISDEGRYFCQLYTPDPQSYTTI 136
QY 121 TVLVPPRLNMDIQKTAVEGEIEVNCVTAMASKPATIRFKGNKELKGKSEVEWSDM 180
Db 137 TVLVPPRLNMDIQKTAVEGEIEVNCVTAMASKPATIRFKGNKELKGKSEVEWSDM 196
QY 181 YTVTSQMLKVHKEDDGVPIVCQVEHPAVTGNLTQRYLEVQYKQVHVH QMTYPLQGLTR 240
Db 197 YTVTSQMLKVHKEDDGVPIVCQVEHPAVTGNLTQRYLEVQYKQVHVH QMTYPLQGLTR 256
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
Db 257 EGDALFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 316
QY 301 VGKAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 317 VGKAHSDYMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
QY 361 GWAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 420

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PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying a nucleotide
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 442 AA;

XX Query Match 98.6%; Score 2166; DB 7; Length 442;

XX Best Local Similarity 98.6%; Pred. No. 3.4e-149;

XX Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFQOLLNFSSELKVSLSLTVNVSISDEGRYFCQLYTDPQESYTTI 120
Db 79 PNRQTIYFRDFRPLKDSRFQOLLNFSSELKVSLSLTVNVSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 180
Db 139 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGVFVICOVEHPAVTGNLQYKYLEVQKPVQVHQMTPYLOGLTR 240
Db 199 YTVTSQMLKVKHEDDGVFVICOVEHPAVTGNLQYKYLEVQKPVQVHQMTPYLOGLTR 258
QY 241 EGDFAELTCEATGKPOVMVTVRVDDEMPQAVLSGPNLFNNLKNKTNGYRCEASNI 300
Db 259 EGDFAELTCEATGKPOVMVTVRVDDEMPQAVLSGPNLFNNLKNKTNGYRCEASNI 318
QY 301 VGKAHSDYMLYVDPPTTPPTTT 360
Db 319 VGKAHSDYMLYVDPPTTPPTTT 378
QY 361 GVVAVVVFAMLCLLIILGYRFARHKGTYFTHBAKGADDAADATAIINAEQQNNSEKK 420
Db 379 GVVAVVVFAMLCLLIILGYRFARHKGTYFTHBAKGADDAADATAIINAEQQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 14
AAV17830

ID AAV17830 standard; protein; 440 AA.
XX AC AAV17830;
XX DT 12-AUG-1999 (first entry)
XX DE Human PRO355 protein sequence.
XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX KW secreted protein; transmembrane protein; inflammation disorder.
XX OS Homo sapiens.
XX FN WO9928462-A2.
XX PD 10-JUN-1999.
XX PF 01-DEC-1998; 98WO-US025108.
XX PR 03-DEC-1997; 97US-0067411P.
XX PR 11-DEC-1997; 97US-0069278P.
XX PR 11-DEC-1997; 97US-0069334P.
XX PR 12-DEC-1997; 97US-0069335P.
XX PR 12-DEC-1997; 97US-0069425P.
XX PR 16-DEC-1997; 97US-0069696P.
XX PR 16-DEC-1997; 97US-0069702P.
XX PR 17-DEC-1997; 97US-0069870P.
XX PR 17-DEC-1997; 97US-0069873P.
XX PR 18-DEC-1997; 97US-0068017P.
XX PR 03-JAN-1998; 98US-0070440P.
XX PR 09-FEB-1998; 98US-0074086P.
XX PR 09-FEB-1998; 98US-0074092P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PA (GETH) GENENTECH INC.
XX PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX WPI; 1999-3711118/31.
XX DR N-PSDB; AAX80055.
XX Nucleic acids encoding PRO secreted and transmembrane proteins.
XX Claim 12; Fig 27; 123pp; English.
XX The present invention describes nucleic acids encoding PRO secreted and
XX transmembrane proteins used therapeutically. The PRO proteins have
XX cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
XX activity. The proteins and polynucleotides can be used in therapy,
XX identification of homologues, raising antibodies and design of probes and
XX primers. They can be used in a range of diseases related to proteins that
XX they have homology with, e.g. a PRO protein having homology to complement
XX proteins may be used in inflammatory responses
XX Sequence 440 AA;
Query Match 97.8%; Score 2149; DB 2; Length 440;
Best Local Similarity 98.3%; Pred. No. 5.8e-148;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
QY 1 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPPG--LRLLLLLSAAALPTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 76
QY 61 PNRQTIYFRDFRPLKDSRFQOLLNFSSELKVSLSLTVNVSISDEGRYFCQLYTDPQESYTTI 120
Db 77 PNRQTIYFRDFRPLKDSRFQOLLNFSSELKVSLSLTVNVSISDEGRYFCQLYTDPQESYTTI 136
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 180
Db 137 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 196

represents a human p53 pathway modifying protein

Sequence 442 AA;

```

every Match      98.6%; Score 2166; DB 6; Length 442;
at Local Similarity 98.6%; Pred. NO. 3.4e-149;
cches 417; Conservative 2; Mismatches 4; Indels

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[illegible]

RESULT 11

ABO07231
ID ABO07231 standard; protein: 442 AA.

AC ABO07231;

DT 13-AUG-2003 (first entry)

DE Human p53 modifying protein, SEQ ID 191.

Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW lung cancer; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PN WO200299122-A1.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 15-FEB-2002; 2002US-0357253P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, Plowman

DR WPI; 2003-156859/15.

N-PSDB; ACD13404.

Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in *Drosophila*.

Example 2; Page 557-559; 678pp; English.

The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in *Drosophila*) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein.

Sequence 442 AA;

Query Match 98.6%; Score 2166; DB 6; Length 442;
 Best Local Similarity 98.6%; Pred. NO. 3.4e-149;
 Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0

[illegible]

XX PD 10-JUL-2003.
 XX PF 18-APR-2001; 2001US-00836353.
 XX PR 28-OCT-1998; 98US-0105971P.
 XX PR 27-OCT-1999; 99MO-US025031.
 XX PR 19-APR-2000; 2000US-0198407P.
 XX PA (NIJJ//) NI J.
 XX PA (YOUN//) YOUNG P E.
 XX PA (KENN//) KENNY J J.
 XX PA (OLSE//) OLSEN H S.
 XX PA (MOOR//) MOORE P A.
 XX PA (WEIY//) WEI Y.
 XX PA (GREE//) GREENE J M.
 XX PA (RUBE//) RUBEN S M.
 XX PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 XX PI Ruben SM;
 XX DR WPI; 2004-020335/02.
 XX PA New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX PA Disclosure; SEQ ID NO 136; 380pp; English.
 XX CC The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 XX SQ Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 8; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AAPPGLRLRLLLLSAALIPGQGNLFKQVTVIEGEVAIVSCVNVKSDSVIQLLN 60
 DB 19 AAPPGLRLRLLLLSAALIPGQGNLFKQVTVIEGEVAIVSCVNVKSDSVIQLLN 78
 QY 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVSLTNVSIISDEGRYFCQLYTDPQESVTTI 120
 DB 79 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVSLTNVSIISDEGRYFCQLYTDPQESVTTI 138
 QY 121 TVLAVPRNLMDIKQTAVERGEIEVNCVTAMASKPATTIRFWKGNKELKGSVEEWSDM 180
 DB 139 TVLAVPRNLMDIKQTAVERGEIEVNCVTAMASKPATTIRFWKGNKELKGSVEEWSDM 198
 QY 181 YTVTSQMLKVKHEDDQVPVICQVEHPAVTGNLTQRYLEVQKPVQHTQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVKHEDDQVPVICQVEHPAVTGNLTQRYLEVQKPVQHTQMTYPLQGLTR 258
 QY 241 EGDALFELTCEAIGKQPFVMVTVRVVDEMPQHAVLSGPNLFINLNKNTDNGTVRCASNI 300
 DB 259 EGDALFELTCEAIGKQPFVMVTVRVVDEMPQHAVLSGPNLFINLNKNTDNGTVRCASNI 318
 QY 301 VGKASDYMLYVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 DB 319 VGKASDYMLYVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
 QY 361 GVAVVVVFMALCLLIILGRYFARHKGTYFTHKAGGADDAADATAIINAEQGNNSSEKK 420
 DB 379 GVAVVVVFMALCLLIILGRYFARHKGTYFTHKAGGADDAADATAIINAEQGNNSSEKK 438
 QY 421 EYF 423

Db 439 EYF 441
 RESULT 10
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 XX AC ABO07196;
 XX DT 13-AUG-2003 (first entry)
 XX DE Human p53 modifying protein, SEQ ID 156.
 XX KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 XX KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 XX KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 XX KW apoptotic disorder; cell proliferation disorder.
 XX OS Homo sapiens.
 XX PN W0200299122-A1.
 XX PD 12-DEC-2002.
 XX PF 03-JUN-2002; 2002WO-US017382.
 XX PR 05-JUN-2001; 2001US-0296076P.
 XX PR 10-OCT-2001; 2001US-0328605P.
 XX PR 15-FEB-2002; 2002US-0357253P.
 XX PA (EXEL-) EXELIXIS INC.
 XX PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX WPI; 2003-156859/15.
 XX DR N-PSDB; ACD13371.
 XX PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 XX Example 2; Page 469-470; 678pp; English.
 XX The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence

139 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 198
181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
241 EGDAPFELTCEAIGKQPQVMTWVRVDDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
259 EGDALFELTCEAIGKQPQVMTWVRVDDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
301 VGKASDVMYVYDPTTIPPTTT 360
319 VGKASDVMYVYDPTTIPPTTT 378
361 GVVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEGGQNNSEKK 420
379 GVVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEGGQNNSEKK 438
421 EYF 423
439 EYF 441

RESULT 8
ADE54238
ID ADE54238 standard; protein; 442 AA.
XX AC ADE54238;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein NP_055148, SEQ ID NO 41.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WC2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2003; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; NP_055148.

PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 7; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGRLRLRLLLLSAALIPITGQNLFTKDVTVIEGEVATISQVNVKSDSDSVIQLLN 60
DB 19 AAPPGRLRLRLLLLSAALIPITGQNLFTKDVTVIEGEVATISQVNVKSDSDSVIQLLN 78
QY 61 PNRQTYFRDPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTYFRDPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 180
DB 139 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKQPQVMTWVRVDDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKASDVMYVYDPTTIPPTTT 360
DB 319 VGKASDVMYVYDPTTIPPTTT 378
QY 361 GVVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEGGQNNSEKK 420
DB 379 GVVAVVVFAMLCILILGRYFARHKGTYFTHKAGDADAADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 9
ADE86685
ID ADE86685 standard; protein; 442 AA.
XX AC ADE86685;
XX DT 29-JAN-2004 (first entry)
XX DE Novel human secreted protein #11 associated protein #1.
XX KW human; secreted protein; cancer; liver disorder; hepatitis;
XX KW neural disorder; Alzheimer's disease.
XX OS Homo sapiens.
XX PN US2003129685-A1.

CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 442 AA;

Query Match
 Best Local Similarity 98.7%; Score 2169; DB 5; Length 442;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 Db 19 AAPGRLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
 QY 61 PNQTIYFRDPRPLKDSRFQLLNFSSSELKVLNTVNSISDEGRYFCQLYTDPQBSYITI 120
 Db 79 PNQTIYFRDPRPLKDSRFQLLNFSSSELKVLNTVNSISDEGRYFCQLYTDPQBSYITI 138
 QY 121 TVLVPRLNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 180
 Db 139 TVLVPRLNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 198
 QY 181 YTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLQTVLEVOYKPOVHIQMTYFLOGLTR 240
 Db 199 YTVTSQMLKVHKEDDGPVVICQVEHPAVTGNLQTVLEVOYKPOVHIQMTYFLOGLTR 258
 QY 241 EGDALFELTCEAIGKPPQVMTWVRVDDMPQHAVLSGNFLNINLKTNDGTYCEASNI 300
 Db 259 EGDALFELTCEAIGKPPQVMTWVRVDDMPQHAVLSGNFLNINLKTNDGTYCEASNI 318
 QY 301 VGKAHSDMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 Db 319 VGKAHSDMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
 QY 361 GVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGQNNSEKK 420
 Db 379 GVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGQNNSEKK 438
 QY 421 EYF 423
 Db 439 EYF 441

RESULT 7
 ADA27144
 ID ADA27144 standard; protein; 442 AA.
 AC ADA27144;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human novel secreted protein from gene 11 #3.
 XX
 KW Cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KW neurological disorder; blood clotting disorder; food additive;
 KW preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 FN US200305231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PE 29-OCT-2001; 2001US-00984130.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.

(NIJ/) NI J.
 (YOUN/) YOUNG P E.
 (KENN/) KENNY J J.
 (OLSE/) OLSEN H S.
 (MOOR/) MOORE P A.
 (WEIY/) WEI Y.
 (GREE/) GREENE J M.
 (RUBE/) RUBEN S M.
 (LIUD/) LIU D.
 (CROC/) CROCKER P R.

NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 Ruben SM, Liu D, Crocker PR;

WPI; 2003-567103/53.

New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting disorders.

Disclosure; Page 72; 454pp; English.

The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridising under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition, or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the invention.

Sequence 442 AA;

Query Match
 Best Local Similarity 98.7%; Score 2169; DB 6; Length 442;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 Db 19 AAPGRLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
 QY 61 PNQTIYFRDPRPLKDSRFQLLNFSSSELKVLNTVNSISDEGRYFCQLYTDPQBSYITI 120
 Db 79 PNQTIYFRDPRPLKDSRFQLLNFSSSELKVLNTVNSISDEGRYFCQLYTDPQBSYITI 138
 QY 121 TVLVPRLNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 180

Db 439 EYF 441

RESULT 5
AAE19887
ID AAE19887 standard; protein; 442 AA.
XX
XX AAE19887;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
DE
XX Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX WO200214557-A1.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US025690.
XX
XX 15-AUG-2000; 2000US-0225264P.
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Reeves RH, Yoshinori M;
XX
XX WPI; 2002-241913/29.
XX
XX Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell
PT of subject with reagent detecting TSLC1 and detecting modification in
PT TSLC1 level.
XX
XX Disclosure; Page 49-50; 59pp; English.
XX
XX The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with a
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1
XX
XX Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 5; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAALIFTGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
DB 19 AAPPGLRLRLLLLSAALIFTGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQIYFRDFRPLKDSRFLNFFSSELKSLTVNVSISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQIYFRDFRPLKDSRFLNFFSSELKSLTVNVSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPRLNLMIDIOKDTAVEGEIEIWNCTAMASKPATIRWPKGNKELKGKSEVEWSDM 180
DB 139 TVLVPRLNLMIDIOKDTAVEGEIEIWNCTAMASKPATIRWPKGNKELKGKSEVEWSDM 198

QY 191 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTCNLOTORYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTCNLOTORYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPPQPMVMTWVRVDDDEMPQHAVLSPNLFINNLTNDNCTYCEASNI 300
DB 259 EGDALFELTCEAIGKPPQPMVMTWVRVDDDEMPQHAVLSPNLFINNLTNDNCTYCEASNI 318
QY 301 VGKASDYMLYVDDPTTIPPTTT 360
DB 319 VGKASDYMLYVDDPTTIPPTTT 378
QY 361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAGGGQNNSEKK 420
DB 379 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAGGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 6
ABP62825
ID ABP62825 standard; protein; 442 AA.
XX
XX AC ABP62825;
XX
XX 14-OCT-2002 (first entry)
XX
XX Human polypeptide SEQ ID NO 262.
XX
XX Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
KW burn; central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; immune disorder;
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
XX Homo sapiens.
XX
XX WO200218424-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027093.
XX
XX 01-SEP-2000; 2000US-00654935.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX WPI; 2002-583321/62.
XX
XX N-PSDB; ABQ93304.
XX
XX New polynucleotide and polypeptides, useful for treatment and diagnosis
PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
PT sclerosis, diabetes and allergies.
XX
XX Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising one of
CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
CC administering to a mammalian subject a composition comprising the protein
CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
CC (I) is useful for gene therapy of diseases and (II) can be used for
CC therapeutic treatment. Diseases that may be treated include wound healing
CC and tissue repair, burns, central nervous system disorders (e.g.
CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral

PI Baum PR, Fanslow WC;
 XX WPI: 2000-205712/18.
 DR N-PSDB; AAZ50883.
 XX Novel molecules designated LDCAM are capable of altering or modulating T
 PT cell function.
 XX
 XX Claim 7; Page 46-47; 44pp; English.
 XX The present amino acid sequence is the mouse lymphoid derived dendritic
 CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
 CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
 CC region of B7-L1. Mouse LDCAM is found on whole embryo, testes, triple
 CC negative cells murine splenic and lymph node CD8+, S49.1 and dendritic
 CC cells. LDCAM polypeptides interact with T cell surface molecules to
 CC alter signalling and inhibits T cell proliferation, bind to themselves
 CC and B7L-1, an LDCAM binding protein and increases natural killer (NK)
 CC cell populations. It may be used to measure the biological activity and
 CC as quality control reagents of LDCAM binding proteins. LDCAM may be used
 CC for treating disorders associated with malfunctioning of immune system,
 CC inflammation, autoimmune disorders, viral infected cells, infectious
 CC diseases and for killing tumour cells. They are also useful for
 CC prevention or reducing the effect of organ and bone marrow transplant
 CC rejection and for modulating T cell immune responses. LDCAM polypeptides
 CC may also be used as carriers for delivering agents attached to T cells or
 CC cells bearing B7L-1
 XX
 XX Sequence 423 AA;

Query Match 100.0%; Score 2197; DB 3; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.8e-151;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 DB 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60

QY 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYTDPDQESYTTI 120
 DB 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYTDPDQESYTTI 120

QY 121 TVLVPPRNLMIDTQKTAVEGEIEVNCNTAMASKPATTIRWFKNKELKGSVEEWSDM 180
 DB 121 TVLVPPRNLMIDTQKTAVEGEIEVNCNTAMASKPATTIRWFKNKELKGSVEEWSDM 180

QY 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQOTQRYLEVOYKPOVHIQMTYFLOGLTR 240
 DB 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQOTQRYLEVOYKPOVHIQMTYFLOGLTR 240

QY 241 EGDAFELTCEAIGKQPQPMVTVRVDDMPQHAVLSPGNLFINLNKTDNGTYRCASNI 300
 DB 241 EGDAFELTCEAIGKQPQPMVTVRVDDMPQHAVLSPGNLFINLNKTDNGTYRCASNI 300

QY 301 VGRAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITLITDSRAGEGTYGAVDHAVIG 360
 DB 301 VGRAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITLITDSRAGEGTYGAVDHAVIG 360

QY 361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGNNEEKK 420
 DB 361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGNNEEKK 420

QY 421 EYF 423
 DB 421 EYF 423

RESULT 2
 AAB25619
 ID AAB25619 standard; protein; 442 AA.
 XX
 AC AAB25619;
 XX

DT 21-NOV-2000 (first entry)
 XX Protein encoded by human secreted protein gene #11.
 DE
 XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.
 XX
 OS Homo sapiens.
 XX WO200029435-A1.
 XX 25-MAY-2000.
 XX 27-OCT-1999; 99WO-US025031.
 XX 28-OCT-1998; 98US-0105971P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;
 XX WPI: 2000-387742/33.
 DR Isolated nucleic acid molecules encoding human secreted proteins are used
 XX for the prevention, amelioration and treatment of autoimmune,
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 PT wounds, and infectious diseases.
 XX Disclosure; Page 182-183; 803pp; English.
 PS The present invention relates to 12 secreted human proteins and the
 CC nucleotide sequences encoding them. The polynucleotide sequences given in
 CC AAA80606-A80623 encode the 12 secreted protein sequences given in
 CC AAB25576-B25593. The human secreted proteins have various activities
 CC dependent on the tissues in which they are expressed. Examples of the
 CC activities of the proteins include: immunosuppressant; anti-inflammatory;
 CC antirheumatic; antiproliferative; dermatological; antiproliferative;
 CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
 CC and antifungal activity. The proteins, polypeptides, agonists and
 CC antagonists may be used to treat prevent and/or diagnose various disease,
 CC disorders and conditions examples of which include: immune disorders e.g.
 CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 CC Crohn's disease and nephritis; hyperproliferative disorders such as
 CC paraproteinemia and purpura; cardiovascular disorders e.g. coronary
 CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
 CC proteins and polynucleotide sequences may also be used in wound healing
 CC and the treatment of infectious diseases. The human secreted protein gene
 CC #11 and protein sequences are represented in sequences AAA80616 and
 CC AAB25586. Sequences AAA80677-A80682 represent genes related to the
 CC secreted protein gene#11
 XX Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 3; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 DB 19 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78

QY 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYTDPDQESYTTI 120
 DB 79 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYTDPDQESYTTI 138

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 48.4142 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title:

Perfect score: 2197

Sequence: 1 APPGLRLRLLLLLLSAAL.....TAIINAEQGNNSSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	3 AAY45093	Aay45093 Mouse Lym
2	2169	98.7	442	3 AAB25619	Aab25619 Protein e
3	2169	98.7	442	3 AAY94341	Aay94341 Human cel
4	2169	98.7	442	3 AAY45092	Aay45092 Human lym
5	2169	98.7	442	5 AAB19887	Aab19887 Human tum
6	2169	98.7	442	5 ABP62825	Abp62825 Human pol
7	2169	98.7	442	6 ADA27144	Ada27144 Human nov
8	2169	98.7	442	7 ADE54238	Ade54238 Human pro
9	2169	98.7	442	8 ABE86685	Abe86685 Novel hum
10	2166	98.6	442	6 AB007196	Ab007196 Human p53
11	2166	98.6	442	6 AB007231	Ab007231 Human p53
12	2166	98.6	442	7 ADE61605	Ade61605 Human pro
13	2166	98.6	442	7 ADE61608	Ade61608 Human pro
14	2149	97.8	440	2 AAY17830	Aay17830 Human PRO
15	2149	97.8	440	3 AAB01321	Aab01321 Human PRO
16	2149	97.8	440	4 AAU29040	Aau29040 Human PRO
17	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
18	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
19	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
20	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
21	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
22	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
23	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
24	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO
25	2149	97.8	440	6 ABUS8416	Abu8416 Human PRO

26	2149	97.8	440	6 ABR68092	AbR68092 Human sec
27	2149	97.8	440	6 ABUS6145	Abu6145 Novel hum
28	2149	97.8	440	6 ABUS6145	Abu6145 Novel hum
29	2149	97.8	440	6 ABO08653	AbO08653 Human sec
30	2149	97.8	440	6 ABO08653	AbO08653 Human sec
31	2149	97.8	440	6 ABO02705	AbO02705 Human sec
32	2149	97.8	440	6 ABR74859	AbR74859 Human sec
33	2149	97.8	440	6 ABR94621	AbR94621 Human sec
34	2149	97.8	440	6 ABUS0240	AbU0240 Human PRO
35	2149	97.8	440	6 ABUS5594	AbU5594 Human PRO
36	2149	97.8	440	6 ABUS5594	AbU5594 Human PRO
37	2149	97.8	440	6 ABUS7969	AbU7969 Novel hum
38	2149	97.8	440	6 ABUS1675	AbU1675 Novel hum
39	2149	97.8	440	6 ABUS9368	AbU9368 Human PRO
40	2149	97.8	440	6 ABUS6209	AbU6209 Human PRO
41	2149	97.8	440	6 ABUS7422	AbU7422 Human sec
42	2149	97.8	440	6 ABUS0450	AbU0450 Human PRO
43	2149	97.8	440	6 ABR99368	AbR99368 Human sec
44	2149	97.8	440	6 ABR98758	AbR98758 Human sec
45	2149	97.8	440	6 ABO16281	AbO16281 Human sec
					AbR92181 Human sec

ALIGNMENTS

RESULT 1

AAAY45093

ID AAY45093 standard; protein; 423 AA.

AC AAY45093;

DT 31-MAY-2000 (first entry)

DE Mouse lymphoid derived dendritic cell adhesion molecule.

KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1;

KW B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;

KW biological activity; quality control reagent; treatment; inflammation;

KW immune system disorder; autoimmune; viral infection; infectious disease;

KW organ transplant rejection; bone marrow; modulator; immune response.

OS Mus sp.

XX

FH Key

FT Domain

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

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FT Modified-site

FT Modified-site

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FT Modified-site

Db 199 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQOTRYLEVQYKQPQVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKQPQPMVTVWRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKQPQPMVTVWRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPPPTTTPPTTT 360
Db 319 VGKASDYMLYVYDPPPTTTPPTTT 378
QY 361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAEAGGONNSEKK 420
Db 379 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAEAGGONNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 15

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 9; Length 440;
Best Local Similarity 98.3%; Pred. No. 8.3e-167;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
QY 1 AAPGRLRLRLLLLSAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
Db 19 AAPPG--LRLLLLFSAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 76
QY 61 PNRQTIYFRDPRFKDSRFLNPFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
Db 77 PNRQTIYFRDPRFKDSRFLNPFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 136
QY 121 TVLVPRLNLMIDIQKDTAVEGEIEVNCNTAMASKPATTIRWFKGNKELKSKSEVEWSDM 180
Db 137 TVLVPRLNLMIDIQKDTAVEGEIEVNCNTAMASKPATTIRWFKGNTELKSKSEVEWSDM 196
QY 181 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQOTRYLEVQYKQPQVHIQMTYPLQGLTR 240
Db 197 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQOTRYLEVQYKQPQVHIQMTYPLQGLTR 256

QY 241 EGDALFELTCEAIGKQPQPMVTVWRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 257 EGDALFELTCEAIGKQPQPMVTVWRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 316
QY 301 VGKASDYMLYVYDPPPTTTPPTTT 360
Db 317 VGKASDYMLYVYDPPPTTTPPTTT 376
QY 361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAEAGGONNSEKK 420
Db 377 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAEAGGONNSEKK 436
QY 421 EYF 423
Db 437 EYF 439

Search completed: May 27, 2004, 09:52:21
Job time : 36.9363 secs


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US-10-015-115-111
; Sequence 111, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Baha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2000-11-13
; PRIOR FILING DATE: 2000-11-17
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-31
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match      98.7%; Score 2169; DB 15; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLRLLLLSAAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
DB 19 AAPPLRLRLRLLLLSAAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 139 TVLVPPRLNLMIDIQKDTAVEGEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198
QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVRYLEVQKPVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVRYLEVQKPVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIKGPQPMVTVWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 300
DB 259 EGDALCELCEAIKGPQPMVTVWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKAHSDYMLVYDPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378

US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Baha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2000-11-13
; PRIOR FILING DATE: 2000-11-17
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-31
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110

Query Match      98.6%; Score 2166; DB 15; Length 442;
Best Local Similarity 98.6%; Pred. No. 3.4e-168;
Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLRLLLLSAAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
DB 19 AAPPLRLRLRLLLLSAAALPTGQGNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 139 TVLVPPRLNLMIDIQKDTAVEGEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198
QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVRYLEVQKPVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVRYLEVQKPVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIKGPQPMVTVWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 300
DB 259 EGDALCELCEAIKGPQPMVTVWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKAHSDYMLVYDPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
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QY 121 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 11

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
DB 19 AAPGLRLRLLLLSAAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 318

QY 301 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 12

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHUI770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
DB 19 AAPGLRLRLLLLSAAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPOQPMVMTWVRVDDMPQHAVLSGPNLFNNLNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKASDYMILVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLIIILGRYFARHKGTYFTHKAGDAADADATAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 13

	Query Match	98.7%	Score 2169	DB 10	Length 442
	Best Local Similarity	98.8%	Pred. No. 2e-168		
	Matches 418	Conservative 1	Mismatches 4	Indels 0	Gaps 0
QY	1	AAPPGRLRLRLLLLSAAALIP	TDGQNLFTKDVT	VEGEVATISQVKNKSDSDV	QTLN 60
Db	19	AAPPGRLRLRLLLLSAAALIP	TDGQNLFTKDVT	VEGEVATISQVKNKSDSDV	QTLN 78
QY	61	PNRQTYFRDRLPKDSRQQLN	FSSESIKVSLTNVSI	DGEGYFCQLYTDPPQESY	TTI 120

QY	121	TVLVPPRLNLMIDIOKOTAVEGEEIEVUNCTAMASKPATTIRWFKGNKELKGKSEVEWSM	180
Db	139	TVLVPPRLNLMIDIOKOTAVEGEEIEVUNCTAMASKPATTIRWFKGNTELKGKSEVEWSM	198
QY	181	YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTKRYLEVOYKPVQVHQMITYPLOGLTR	240
Db	199	YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTKRYLEVOYKPVQVHQMITYPLOGLTR	258
QY	241	EGDAPELTCFAIGKPPQPMVTVWRVDDMPQHAVLSGNPLFINLNKTDNGTYRCEASNI	300
Db	259	EGDALELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGNPLFINLNKTDNGTYRCEASNI	318
QY	301	VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTITITDTSRAGEEGTIGAVDHAVTG	360
Db	319	VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTITITDTSRAGEEGSIRAVDHAVTG	378
QY	361	GVAVVVFVFMCLLLIILGRVFARHKGTFTFHEAKGADDAADATATINAEKGONNSEKK	420
Db	379	GVAVVVFVFMCLLLIILGRVFARHKGTFTFHEAKGADDAADATATINAEKGONNSEKK	438
QY	421	EYF 423	
Db	439	EYF 441	

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RESULT 10
US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262

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Query Match	98.7%;	Score 2169;	DB 12;	Length 442;
Best Local Similarity	98.8%;	Pred. No. 2e-168;		
Matches 418;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	AAPGLRLRLULLLSAALI	PTGDCQNLF	TKDVTVIEGEVATIS
		QVVKVQVQVQVQVQVQVQV	QVVKVQVQVQVQVQVQV	QVVKVQVQVQVQVQVQV
DB	19	AAPGLRLRLULLLSAALI	PTGDCQNLF	TKDVTVIEGEVATIS
		QVVKVQVQVQVQVQVQVQV	QVVKVQVQVQVQVQVQV	QVVKVQVQVQVQVQVQV
QY	61	PNRQTIYFRFLKDSRFL	KNFSSELK	VSITNVSIDEGRYFC
		LYTDPQESYTTI		
DB	79	PNRQTIYFRFLKDSRFL	KNFSSELK	VSITNVSIDEGRYFC
		LYTDPQESYTTI		

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Db 300 EGDAPFELTCEAIGKQPQVMVTVRVVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 359
QY 301 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
Db 360 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 419
QY 350 TIGAVDHAVIGGVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINA 409
Db 420 TIGAVDHAVIGGVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINA 479
QY 410 EGGQNNSEKKEYF 423
Db 480 EGGQNNSEKKEYF 493

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RESULT 6

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:

APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-778-510-20

Query Match
Best Local Similarity 98.7%; Score 2169; DB 9; Length 442;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AAPPGLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 60
Db 19 AAPPGLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 78
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSSELKVSLSLNVSISDEGRYFCQLYTDPPOESYTTI 120
Db 79 PNRQTIYFRDPRPLKDSRFQQLNFSSSELKVSLSLNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRNLMDIQKTAVGEIEVNVCTAMASKPATTTIRWFKGNTELKKGSEVEWSDM 180
Db 139 TVLVPPRNLMDIQKTAVGEIEVNVCTAMASKPATTTIRWFKGNTELKKGSEVEWSDM 198
QY 181 YTVTSQMLVKHKEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLVKHKEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQVMVTVRVVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
Db 259 EGDAPFELTCEAIGKQPQVMVTVRVVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 420
Db 379 GVVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

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RESULT 7

US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens

Query Match
Best Local Similarity 98.7%; Score 2169; DB 9; Length 442;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AAPPGLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 60
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Db 79 PNRQTIYFRDPRPLKDSRFQQLNFSSSELKVSLSLNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRNLMDIQKTAVGEIEVNVCTAMASKPATTTIRWFKGNTELKKGSEVEWSDM 180
Db 139 TVLVPPRNLMDIQKTAVGEIEVNVCTAMASKPATTTIRWFKGNTELKKGSEVEWSDM 198
QY 181 YTVTSQMLVKHKEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLVKHKEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQVMVTVRVVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
Db 259 EGDAPFELTCEAIGKQPQVMVTVRVVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKASDYMVLVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 420
Db 379 GVVAVVAVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

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RESULT 8

US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US2003005231A1
; GENERAL INFORMATION:
APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PP489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792

GENERAL INFORMATION:

APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangolli, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 112
LENGTH: 445
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-112

Query Match 100.0%; Score 2197; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
DB 22 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 81
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSITNVISDEGRYFCQLYTDPPQESYTTI 120
DB 82 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSITNVISDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201
QY 181 YTVTSQMLKVKHKEDDGVPIQVQHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
DB 202 YTVTSQMLKVKHKEDDGVPIQVQHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
DB 262 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 321
QY 301 VGKASDVMYLVYDPTTTPPTTT 360
DB 322 VGKASDVMYLVYDPTTTPPTTT 381
QY 361 GVAVVVFAMCLLLIILGRYFARHKGTYFTEAKGADDAADATAIINAEQGNNSSEKK 420
DB 382 GVAVVVFAMCLLLIILGRYFARHKGTYFTEAKGADDAADATAIINAEQGNNSSEKK 441

QY 421 EYF 423
DB 442 EYF 444

RESULT 5

US-10-015-115-113
Sequence 113, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangolli, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 113
LENGTH: 494
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-113

Query Match 99.1%; Score 2176.5; DB 15; Length 494;
Best Local Similarity 97.2%; Pred. No. 5.6e-169;
Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
DB 60 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 119
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSITNVISDEGRYFCQLYTDPPQESYTTI 120
DB 120 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSITNVISDEGRYFCQLYTDPPQESYTTI 179
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 180 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 239
QY 181 YTVTSQMLKVKHKEDDGVPIQVQHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
DB 240 YTVTSQMLKVKHKEDDGVPIQVQHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 299
QY 241 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300

QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
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QY 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
Db 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423
RESULT 2
US-09-778-187B-4
; Sequence 4, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: mus musculus
US-09-778-187B-4
Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSNTVNSISDEGRYFCOLYTDPPQESYTTI 120
Db 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSNTVNSISDEGRYFCOLYTDPPQESYTTI 120
QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEBWSM 180
Db 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEBWSM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
Db 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
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Db 241 EGDAPFELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
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QY 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
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QY 421 EYF 423
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US-10-015-115-112
; Sequence 112, Application US/10015115
; Publication No. US20030207800A1

Db 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423
RESULT 3
US-10-302-041-22
; Sequence 22, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B711
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-302-041-22
Query Match 100.0%; Score 2197; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSNTVNSISDEGRYFCOLYTDPPQESYTTI 120
Db 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSNTVNSISDEGRYFCOLYTDPPQESYTTI 120
QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEBWSM 180
Db 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEBWSM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
Db 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
QY 241 EGDAPFELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
Db 241 EGDAPFELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
QY 301 VGKASHDYMLYVDDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 301 VGKASHDYMLYVDDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
QY 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
Db 361 GVAVVVFAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 35.9363 seconds
(without alignments)
3286.999 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPPGRLRLLLLLLSAAAL.....TAIINAEGQNNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA.*

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- 13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2197	100.0	423	9	US-09-778-187B-4
3	2197	100.0	423	14	US-10-302-041-22
4	2197	100.0	445	15	US-10-015-115-112
5	2176.5	99.1	494	15	US-10-015-115-113
6	2169	98.7	442	9	US-09-778-510-20
7	2169	98.7	442	9	US-09-778-187B-2
8	2169	98.7	442	10	US-09-984-130-136
9	2169	98.7	442	10	US-09-836-353A-136
10	2169	98.7	442	12	US-10-363-616-262
11	2169	98.7	442	14	US-10-302-041-20
12	2169	98.7	442	14	US-10-403-107-1
13	2169	98.7	442	15	US-10-015-115-111
14	2166	98.6	442	15	US-10-015-115-110
15	2149	97.8	440	9	US-09-866-028-61

16	2149	97.8	440	9	US-09-944-449-61	Sequence 61, Appl
17	2149	97.8	440	9	US-09-944-457-61	Sequence 61, Appl
18	2149	97.8	440	9	US-09-944-862-61	Sequence 61, Appl
19	2149	97.8	440	9	US-09-945-587-61	Sequence 61, Appl
20	2149	97.8	440	9	US-09-945-587-61	Sequence 61, Appl
21	2149	97.8	440	9	US-09-944-396-61	Sequence 61, Appl
22	2149	97.8	440	9	US-09-944-097-61	Sequence 61, Appl
23	2149	97.8	440	9	US-09-944-432-61	Sequence 61, Appl
24	2149	97.8	440	9	US-09-943-762-61	Sequence 61, Appl
25	2149	97.8	440	9	US-09-944-654-61	Sequence 61, Appl
26	2149	97.8	440	9	US-09-943-851A-61	Sequence 61, Appl
27	2149	97.8	440	9	US-09-944-413-61	Sequence 61, Appl
28	2149	97.8	440	9	US-09-944-403-61	Sequence 61, Appl
29	2149	97.8	440	9	US-09-944-896-61	Sequence 61, Appl
30	2149	97.8	440	9	US-09-944-944-61	Sequence 61, Appl
31	2149	97.8	440	9	US-09-944-929-61	Sequence 61, Appl
32	2149	97.8	440	9	US-09-944-907-61	Sequence 61, Appl
33	2149	97.8	440	10	US-09-944-884-61	Sequence 61, Appl
34	2149	97.8	440	10	US-09-944-852-61	Sequence 61, Appl
35	2149	97.8	440	10	US-09-943-780-61	Sequence 61, Appl
36	2149	97.8	440	11	US-09-945-584-61	Sequence 61, Appl
37	2149	97.8	440	12	US-10-206-915-34	Sequence 34, Appl
38	2149	97.8	440	12	US-10-199-670-34	Sequence 34, Appl
39	2149	97.8	440	12	US-10-201-858-34	Sequence 34, Appl
40	2149	97.8	440	12	US-10-205-890-34	Sequence 34, Appl
41	2149	97.8	440	12	US-10-208-024-34	Sequence 34, Appl
42	2149	97.8	440	12	US-10-201-853-34	Sequence 34, Appl
43	2149	97.8	440	12	US-10-677-471-61	Sequence 61, Appl
44	2149	97.8	440	12	US-10-677-669-61	Sequence 61, Appl
45	2149	97.8	440	12	US-10-174-581-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-22 ; Sequence 22, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171; Indels 0; Gaps 0;
Matches 423; Conservative 0; Mismatches 0;

QY	1	AAPPGRLRLLLLLLSAAALIFTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLIN	60
Db	1	AAPPGRLRLLLLLLSAAALIFTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLIN	60
QY	61	PNRQIYFRDPRPLKDSRFQLNFFSSSELKVSILTNVSI DGRYFCQLYTDPQBSYTTI	120
Db	61	PNRQIYFRDPRPLKDSRFQLNFFSSSELKVSILTNVSI DGRYFCQLYTDPQBSYTTI	120
QY	121	TVLVPRLNLMIDIQDXTAVEGEIEIWNCTAMASKATTIRWFKGNKELKGKSEVEWSDM	180
Db	121	TVLVPRLNLMIDIQDXTAVEGEIEIWNCTAMASKATTIRWFKGNKELKGKSEVEWSDM	180

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Db 61 KVHEDDGPVVICQVEHPAVTGNLTQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 120
Qy 250 EAIGKPOQVMVTVWRVDDMEQHAVLSGNPLFINNLANKTNGTYRCEASNIVGKASDYM 309
Db 121 EAIGKPOQVMVTVWRVDDMEQHAVLSGNPLFINNLANKTNGTYRCEASNIVGKASDYM 180
Qy 310 LYVYDPTTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAVIGGVAVVVA 369
Db 181 LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDHAVIGGVAVVVA 223
Qy 370 MLCILLILGRYFARHKGTYFTHKAGDAADADATAIINAEQQNNSEKKEYF 423
Db 224 MLCILLILGRYFARHKGTYFTHKAGDAADADATAIINAEQQNNSEKKEYF 277

RESULT 15
Q8N3J6
ID Q8N3J6 PRELIMINARY; PRT; 435 AA.
AC Q8N3J6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKZP761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgam;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00815; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 40.8%; Score 897; DB 4; Length 435;
Best Local Similarity 44.2%; Pred. No. 1.5e-67;
Matches 192; Conservative 75; Mismatches 139; Indels 28; Gaps 7;

Qy 11 LLLLLSAAALIPTC-DGQNLFTKDVTVIEGVATISQVKNKSDSVIQLNPNRQTIYFR 69
Db 8 VLRFSVCGLLQSQGQFFLTQNVTVVGGTALTCTCRVDNDNTSLQWSNPAQQTLYFD 67
Qy 70 DFRPLKDSRFQLNLFSSSELKSLVSTNVSISDEGRYFCQLYTDPPQSYTTITVLVPPNL 129
Db 68 DKXALDRNRIELVRASWHELISVSDSDEGGYTCSLFTMPVKTSKAYLTVLGVPEKP 127
Qy 130 MIDIQKDTAVEGEEIEVNCAMASKPATITRFPKGNKELKKGSEVEWS---DMYTVTSQ 186
Db 128 QISGFSPPVMEGLMQLTCKTSGSKPAADIRWFKNDKEIKDVYKLEEDANRKTFTVSST 187
Qy 187 LMLKVHKEDGVPVICQVEHPAVTGNLTQRYLEVQKPVQVHIQMTYPLQGLTREGDAF 245
Db 188 LDFRVRSDGVAICVDRHESNATPQVAMQVLEIHYTPSVKI---IPSTPPPGQPL 244
Qy 246 ELTCEAIGKFPQPVVWTVWRVDDME--PQHAVLSGNPLFINNLANKTNGTYRCEASNIVGK 303
Db 245 ILACESKGLPEPVLWTKDGGELPDPDRNVSGRELNLFLNKTNGTYRCEATNTIGQ 304
Qy 304 AHSYMLYVYDPTTPIPPPTTTTTTTTTTTTTTTTTTTTTIT 349
Db 305 SSAEYVLIVHDVENTLIPTIIPSLTATVTTTVAITTSPTTSATTSISDNPALAGQNG 364
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Qy 350 TIGAVDHAIVGGVAVVVFAMLCILLILGRYFARHKGTYFTHKAGDAADADADTAIINA 409
Db 365 P-----DHALLGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINA 420
Qy 420 EGGQNNSEKKEYF 423
Db 421 EGSQVNAEKKKEYF 434

Search completed: May 27, 2004, 09:34:56
Job time : 35.688s secs
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DR GO: GO:0005515; P:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 235 AA; 32347 MW; FDD9B8145C6B971B CRC64;

Query Match 68.0%; Score 1493; DB 11; Length 295;
 Best Local Similarity 96.6%; Pred. No. 2.3e-118;
 Matches 284; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 130 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQYLYEVQKPOVHIQMTYPLQGLTREGDAFELTC 249
 Db 61 KVHKEDGVPVICOVEHPAVTGNLQYLYEVQKPOVHIQMTYPLQGLTREGDAFELTC 120
 QY 250 EAIGKPOPMVTVVRVDEMPQHAVLSPNLFNNLNKTDTNGTYRCEASNVGKAHSDYM 309
 Db 121 EAIGKPOPMVTVVRVDEMPQHAVLSPNLFNNLNKTDTNGTYRCEASNVGKAHSDYI 180
 QY 310 LYVYDPTTTPPPPTTT 369
 Db 181 LYVYDPTTTPPPPTTT 240
 QY 370 MLCLLIILGRYFARHKGTFTYTHAKGADDAADATAIINAEGGNNSEKKEYF 423
 Db 241 MLCLLIILGRYFARHKGTFTYTHAKGADDAADATAIINAEGGNNSEKKEYF 294

RESULT 13

Q09YL5
 ID Q09YL5 PRELIMINARY; PRT; 289 AA.
 AC Q09YL5;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175B.
 GN IGSF4 OR RAI175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D00565AE4 CRC64;

Query Match 63.9%; Score 1404; DB 11; Length 289;
 Best Local Similarity 92.5%; Pred. No. 7.9e-111;
 Matches 272; Conservative 2; Mismatches 14; Indels 6; Gaps 1;

QY 130 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQYLYEVQKPOVHIQMTYPLQGLTREGDAFELTC 249
 Db 61 KVHKEDGVPVICOVEHPAVTGNLQYLYEVQKPOVHIQMTYPLQGLTREGDAFELTC 120
 QY 250 EAIGKPOPMVTVVRVDEMPQHAVLSPNLFNNLNKTDTNGTYRCEASNVGKAHSDYM 309
 Db 121 EAIGKPOPMVTVVRVDEMPQHAVLSPNLFNNLNKTDTNGTYRCEASNVGKAHSDYI 180
 QY 310 LYVYDPTTTPPPPTTT 369
 Db 181 LYVYDPTTTPPPPTTT 234
 QY 370 MLCLLIILGRYFARHKGTFTYTHAKGADDAADATAIINAEGGNNSEKKEYF 423
 Db 235 MLCLLIILGRYFARHKGTFTYTHAKGADDAADATAIINAEGGNNSEKKEYF 288

RESULT 14

Q09YL3
 ID Q09YL3 PRELIMINARY; PRT; 278 AA.
 AC Q09YL3;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175N.
 GN IGSF4 OR RAI175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021967; BAA87917.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

Query Match 62.8%; Score 1380.5; DB 11; Length 278;
 Best Local Similarity 90.8%; Pred. No. 7.4e-109;
 Matches 267; Conservative 2; Mismatches 8; Indels 17; Gaps 1;

QY 130 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQYLYEVQKPOVHIQMTYPLQGLTREGDAFELTC 249


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QY 161 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 240
DB 202 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 261
QY 241 EGDAPFLTCEALGKQPQVWVWVRVDDMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
DB 262 EGDAPFLTCEALGKQPQVWVWVRVDDMPQHAVLSGNLFINNLTNDNGTYRCEASNI 321
QY 301 VGKASHDMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 322 VGKASHDMLYVY-----DSRAGEEGTICAVDHAIVG 353
QY 361 GVVAVVVFAMLCIIILGRYPARHKGTFTTHEAKGADDAADATTAIINAGGQNNSEKK 420
DB 354 GVVAVVVFAMLCIIILGRYPARHKGTFTTHEAKGADDAADATTAIINAGGQNNSEKK 413
QY 421 EYF 423
DB 414 EYF 416

RESULT 6
Q8N2F4
ID Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC Q8N2F4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Embryo.
RC Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR ENBL; AK013775; BAB28988.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG2; 3.
DR SMART; SM00408; IG2; 3.
DR PROSITE; PS0835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

Query Match 92.0%; Score 2020.5; DB 4; Length 443;
Best Local Similarity 92.9%; Pred. No. 6.9e-163;
Matches 394; Conservative 5; Mismatches 24; Indels 1; Gaps 1;

QY 1 AAPGLRLRLLLLSAALIPCTGQNLFPKQVTVIEGEVATISQVKNKSDSDSVIQLIN 60
DB 19 AAPGLRLRLLLLSAALIPCTGQNLFPKQVTVIEGEVATISQVKNKSDSDSVIQLIN 78
QY 61 PNQTIYFRDPRPLKDSRFQQLNFSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNQTIYFRDPRPLKDSRFQQLNFSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPNLMIDIKQTAVERGEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 180
DB 139 TVLVPPNLMIDIKQTAVERGEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFLTCEALGKQPQVWVWVRVDDMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300

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DB 259 EGDAPFLTCEALGKQPQVWVWVRVDDMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKASHDMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 359
DB 319 VGKASHDMLYVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 360 GVVAVVVFAMLCIIILGRYPARHKGTFTTHEAKGADDAADATTAIINAGGQNNSEKK 419
DB 379 GVVAVVVFAMLCIIILGRYPARHKGTFTTHEAKGADDAADATTAIINAGGQNNSEKK 438
QY 420 KEYF 423
DB 439 KEYF 442

RESULT 7
Q9D6E7
ID Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2900073G06Rik protein.
GN IGSF4 OR 2900073G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR ENBL; AK013775; BAB28988.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IG2; 1.
DR PROSITE; PS0835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FF887FAF4BFDF120 CRC64;

Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 99.1%; Score 2176.5; DB 11; Length 456;
 Best Local Similarity 97.2%; Pred. No. 4.1e-176;
 Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 22 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 81
 QY 61 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 142 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201
 QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
 DB 202 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 261
 QY 241 EGDAPFELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
 DB 262 EGDAPFELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 321
 QY 301 VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
 DB 322 VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 381
 QY 350 TIGAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINA 409
 DB 382 TIGAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINA 441
 QY 410 EGGQNNSEKKEYF 423
 DB 442 EGGQNNSEKKEYF 455

RESULT 4
 Q9BY67 PRELIMINARY; PRT; 442 AA.

ID Q9BY67
 AC Q9BY67
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN NECL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin
 RT superfamily."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132811; AAF69029.1; -.
 DR Genew; HGNC:5951; IGSP4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PSS0835; IGLIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 98.6%; Score 2166; DB 4; Length 442;
 Best Local Similarity 98.6%; Pred. No. 3.1e-175;
 Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 19 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
 QY 61 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 139 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198
 QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
 QY 241 EGDAPFELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
 DB 259 EGDAPFELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
 QY 301 VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 DB 319 VGKAHSDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
 QY 361 GVAVVVFAMLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 420
 DB 379 GVAVVVFAMLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 438
 QY 421 EYF 423
 DB 439 EYF 441

RESULT 5
 Q7TNL1 PRELIMINARY; PRT; 417 AA.

ID Q7TNL1
 AC Q7TNL1
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Nectin-like molecule 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
 RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
 RT "Implications of nectin-like molecule
 RT 2/IGSF4/RA175/SGISF/TSCL1/SyncM1 in cell-cell adhesion and
 RT transmembrane protein localization in epithelial cells."
 RL J. Biol. Chem. 0:0-0(2003).
 DR EMBL; AY351388; AAQ02381.1; -.
 SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

Query Match 92.3%; Score 2027; DB 11; Length 417;
 Best Local Similarity 93.4%; Pred. No. 1.8e-163;
 Matches 395; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

QY 1 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 22 AAPPGLRLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 81
 QY 61 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRTIYFRDPRPLKDSRFQQLNFSSSELKSVLTNVSISDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 142 TVLVPPRLNLMIDIQDRTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201

	Matches	423;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	AAPGLRLRLLLLLSAAALPTGDGQNLFKDVTVIEGEVATISCVWNKSDDSVIQLLN	60							
Dd	22	AAPGLRLRLLLLLSAAALPTGDGQNLFKDVTVIEGEVATISCVWNKSDDSVIQLLN	81							
Qy	61	PNRTIYPRDRPLKDSRFOLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI	120							
Dd	82	PNRTIYPRDRPLKDSRFOLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI	141							
Qy	121	TVLVPPNLMIDIQKTAVEGEELEVNTAMASKPATTIRWKGKNGELKGGSEVEEWSDM	180							
Dd	142	TVLVPPNLMIDIQKTAVEGEELEVNTAMASKPATTIRWKGKNGELKGGSEVEEWSDM	201							
Qy	181	YTVTSQMLMKVKHEDDGPVPVCQVEHPAVTGNLQRYLEYVQYKPVHIQMTYPLOQLTR	240							
Dd	202	YTVTSQMLMKVKHEDDGPVPVCQVEHPAVTGNLQRYLEYVQYKPVHIQMTYPLOQLTR	261							
Qy	241	EGDAFELTCGAIGKQPQPMVTWRVDDEMPOHAVLSGPNLFINNLKNTDNGTYRCASN	300							
Dd	262	EGDAFELTCGAIGKQPQPMVTWRVDDEMPOHAVLSGPNLFINNLKNTDNGTYRCASN	321							
Qy	301	VGKAHSYMLVYDDPPTIPPTTTTTTTTTTTTTTTTTITITDSRAGEGTIGAVDHAVIG	360							
Dd	322	VGKAHSYMLVYDDPPTIPPTTTTTTTTTTTTTTTTTITITDSRAGEGTIGAVDHAVIG	381							
Qy	361	GVAVVVFAMCLLIILGRYPARHKGYFTHEAKGADDAADATAIINAEQQNNSEKK	420							
Dd	382	GVAVVVFAMCLLIILGRYPARHKGYFTHEAKGADDAADATAIINAEQQNNSEKK	441							
Qy	421	EYF 423								
Dd	442	EYF 444								

RESULT 2

```

Q8K3T6      PRELIMINARY;          PRT;    445 AA.
ID   Q8K3T6
AC   Q8K3T6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DI   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Synaptic cell adhesion molecule 1.
GS   IGSF4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN   SEQUENCE FROM N.A.
RP   STRAIN=C57BL/
RA   Biedrer T.B., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
RA   Sudhof T.C.;
RT   "SynCAM, a synaptoblastic adhesion molecule that drives synapse assembly.";
RL   Science 0:0-0(2002).
EMBL; AF539424; AAN01614.1; -.
DR   MGD; MG1.1889272; Igsf4.
CO   GO:0045302; C:synaptic junction; IDA.
DR   GO:0008021; C:synaptic vesicle; IDA.
GO   GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR   GO:0005515; F:protein binding; IPI.
DR   GO:0007155; P:cell adhesion; IDA.
DR   GO:0007416; P:synaptogenesis; IDA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
PFam; PF00047; Ig_3.
SMART; SM00409; IG_3.
SMART; SM00408; IGC2; 3.
DR   PROSITE; PS00835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

```

Query Match					
Best Local Similarity 99.8%; Score 2193; DB 11; Length 445;					
Matches 422; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	AAPGLRLRLVLLILLISAAALPTGDGQNLFKDVTVTVEGEVATISCQVNKSDDSVTQLLN	60		
Dd	22	AAPGLRLRLVLLILLISAAALPTGDGQNLFTKDVTVIIEGVATISCQVNKSDDSVTQLLN	81		
QY	61	PNRQTIFYRDFRPLKDSRFOLLNPFSSSELKVSLTNVSISDEGRYFCOLYTDPPQSYYTI	120		
Dd	82	PNRQTIFYRDFRPLKDSRFOLLNPFSSSELKVSLTNVSISDEGRYFCOLYTDPPQSYYTI	141		
QY	121	TVLVPPRNLMIDIOKDTAVEGEEIENVCTAMASKPATIRWFGKNELKGKSEVEWSDM	180		
Dd	142	TVLVPPRNLMIDIOKDTAVEGEEIENVCTAMASKPATIRWFGKNELKGKSEVEWSDM	201		
QY	181	YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGMLQTORYLEVOYKPQVHIQMTYPIQGLTR	240		
Dd	202	YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGMLQTORYLEVOYKPQVHIQMTYPIQGLTR	261		
QY	241	EGDAFELTCEAIGKQPQVMVTVWVDDEMPQHAVLSGGPNLFINNKDNGTYRCEASNI	300		
Dd	262	EGDAFELTCEAIGKQPQVMVTVWVDDEMPQHAVLSGGPNLFINNKDNGTYRCEASNI	321		
QY	301	VGKAHSDYMLXVYDPPTIPPTTTTTTTTTTTTTTTITLTITSRAGEBGTIGAVDHAVIG	360		
Dd	322	VGKAHSDYMLXVYDPPTIPPTTTTTTTTTTTTTTTITLTITSRAGEBGTIGAVDHAVIG	381		
QY	361	GVAVVVVFAMLCIIILIGRYFARHGKYFTHEAKGADDAADTAIINAEQQNNSEKK	420		
Dd	382	GVAVVVVFAMLCIIILIGRYFARHGKYFTHEAKGADDAADTAIINAEQQNNSEKK	441		
QY	421	EYF 423			
Dd	442	EYF 444			
RESULT 3					
Q8RSMB PRELIMINARY; PRT; 456 AA.					
ID	Q8RSMB				
AC	Q8RSMB				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	RA175.				
GN	IGSF4 OR RA175.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Monoi T.;				
RT	"Biological function of RA175, a new member of immunoglobulin super family.";				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AB064265; BAB83501.2; -.				
DR	MGI; MGI:1869272; Igsf4.				
DR	GO; GO:0045202; C:synaptic vesicle; IDA.				
DR	GO; GO:0008021; C:synaptic junction; IDA.				
DR	GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.				
DR	GO; GO:0005515; F:protein binding; IPI.				
DR	GO; GO:0007155; P:cell adhesion; IDA.				
DR	GO; GO:0007416; P:synaptogenesis; IDA.				
DR	InterPro; IPRO07110; Ig-like.				
DR	InterPro; IPRO03598; Ig_c2.				
DR	InterPro; IPRO03585; Neurexin-like.				
DR	Ffam; PF00047; ig; 3.				
DR	SMART; SM00294; 4.1m; 1.				
DR	SMART; SM00408; IGC2; 1.				
DR	PROSITE; PS50835; IG_LIKE; 3.				
KW	Immunoglobulin domain.				
SQ	SEQUENCE 456 AA; 493787 MW; 322EB866A4BC1C7F CRC64;				

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 34.6885 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPGLRLRLILLLSAAL.....TAIINAEQQNSSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_muc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2197	100.0	445	11	Q84L1 mus musculus
2	2193	99.8	445	11	Q8K3T6
3	2176.5	99.1	456	11	Q85M8
4	2166	98.6	442	4	Q9B67
5	2027	92.3	417	11	Q7TNL1
6	2020.5	92.0	443	4	Q8N2F4
7	1631	74.2	336	11	Q9D6E7
8	1631	74.2	336	11	Q80VG4
9	1615	73.5	333	4	Q86WB8
10	1545	70.4	295	11	Q922H8
11	1513.5	68.9	306	11	Q9QYL4
12	1493	68.0	295	11	Q9QYL6
13	1404	63.9	289	11	Q9QYL5
14	1380.5	62.8	278	11	Q9QYL3
15	897	40.8	435	4	Q8N3J6
16	895	40.7	437	4	Q81ZP8

17	864	39.3	404	11	Q8BLQ9
18	860	39.1	404	11	Q8BYP1
19	857	39.0	395	11	Q8BXJ7
20	854	38.9	395	11	Q8BZP4
21	800	36.4	394	13	Q7ZXX1
22	766.5	34.9	388	4	Q8NFZ8
23	757.5	34.5	388	11	Q8R464
24	739.5	33.7	396	11	Q9N28
25	732.5	33.3	398	4	Q8N126
26	730.5	33.2	381	4	Q9Y4A4
27	715.5	32.6	432	4	Q9UJF1
28	371.5	16.9	163	11	Q8KIH8
29	362.5	16.5	163	4	Q9NVJ5
30	360.5	16.4	152	11	Q8BSQ8
31	337.5	15.4	549	11	Q9D006
32	334.5	15.2	549	11	Q9JLB9
33	325.5	14.8	549	4	Q9NQS3
34	323	14.7	234	4	Q81ZQ9
35	303.5	13.8	438	11	Q9JLB7
36	303.5	13.8	510	11	Q9JLB8
37	283	12.9	439	13	Q57349
38	270	12.3	407	4	Q9Y412
39	263	12.0	1482	5	Q9V4Y0
40	261.5	11.9	5175	5	Q810L3
41	261.5	11.9	5198	5	O76518
42	248.5	11.3	624	11	Q8CIJ4
43	248.5	11.3	789	11	Q80W68
44	247.5	11.3	467	11	Q91VT9
45	247.5	11.3	510	4	Q96NY8

ALIGNMENTS

RESULT 1

Q8R4L1 ID Q8R4L1 PRELIMINARY; PRT; 445 AA.
AC Q8R4L1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Tumor suppressor in lung cancer 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT Identification of murine orthologue of the TSLC1 gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF434663; AAL86736.1; -
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;
Query Match 100.0%; Score 2197; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.3e-178;

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PT DOMAIN 135 233 IG-LIKE C2-TYPE 2.
PT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
PT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
PT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
PT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
PT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
PT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
PT DOMAIN 941 1025 FIBROECTIN TYPE-III.
PT DISULFID 53 111 POTENTIAL.
PT DISULFID 160 217 POTENTIAL.
PT DISULFID 265 317 POTENTIAL.
PT DISULFID 361 417 POTENTIAL.
PT DISULFID 465 528 POTENTIAL.
PT DISULFID 567 623 POTENTIAL.
PT DISULFID 761 816 POTENTIAL.
PT DISULFID 863 920 POTENTIAL.
PT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 547 547 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 553 553 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 564 564 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 577 577 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 680 680 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 708 708 N-LINKED (GLCNAC. .) (POTENTIAL).
PT CARBOHYD 908 908 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 134890 MW; 02D82180BF145092 CRC64;

Query Match 10.1%; Score 221; DB 1; Length 1242;
Best Local Similarity 22.7%; Pred. No 4e-08;
Matches 86; Conservative 75; Mismatches 164; Indels 54; Gaps 16;

QY 5 GLRLRLLLLSAAALPTGDGQ-----LFTKDVTVIEGEVATISQVKNKSD 53
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
4 GTTLRASLL--AGMLTTGLAQSPVPTSA PRGFALSENLTVEGSTIKLWGV-RAPG 59
QY 54 SVIQ-----LLNPNQTIYFRDPRFKDSRFOLLNFSSELKVLSTNVSISDEGRYFCQ 107
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
60 SVVQWAKDGLLGPKNPKIPGFPYSLGDS-----AKGEFHLLEACDLSDDAEYEQ 112
QY 108 LYTDP--PQ--ESYTTITVLVPPRLMIDIQD---TAVEGEIEVNCCTAMASKPATIR 160
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
113 VGRSELGPVLSPRVLSVLVPPKVLQLPFAGSTVTVAGQEVVTVCSGGAKPAPDII 172
QY 161 WPKGNKELKG-KSEVEWSD--MYTTSQMLKVKHKEDDGPVFCQVHPAVTGNLQTOR 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
173 FIQGGRTVEDVSSVNEGSEKLFTEAEARVTPQSSDNGQLLVCEGSPALATPIKASF 232
QY 218 YLEVOYKQVHIQMTYP--LOGLTREGDAFELTCEAIGKPOPVMVTVVRVDEM-----P 270
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
233 TNNILFPGPVPV-IDWFLNEGHRVAGENLELFCIARGGNPPATLQWLKNGKRPVSIAMGT 291
QY 271 QHVLGSPNLFNNLNKTNGT--YRCEASIVGKAHSDYMLVYDDPTTIPPTTT---- 325
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
292 EHAQVAHSLVMTVRPEDHGARLSCQSYNSVAETQERSITL---QVTFPFSAVTILGS 348
QY 326 TTTTITTTTITLITIDSR 344
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
349 TSQSENKNVTLCLTKSSR 367
```

Search completed: May 27, 2004, 09:35:44
Job time : 10.9841 secs

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1092
FT
FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1092
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 208 295
FT DOMAIN 303 397
FT DOMAIN 400 489
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118082 MW; CD236E0E9F87AD1 CRC64;
Query Match 10.1%; Score 222; DB 1; Length 1092;
Best Local Similarity 23.9%; Pred. No. 2.9e-08;
Matches 81; Conservative 68; Mismatches 150; Indels 40; Gaps 15;
QY 32 KDVTVEGEVATISC---QVNS---DVSQVLN-----PQRQIYFRDFPLKDSRFL 81
Db 199 KDIQIVNVPLQARQIRVATNAMDSEVLSCDADGFPDPPEISWLKKGSPIDEGE-EK 257
QY 82 LNFSSSELKSLTNVSIISDEGRYFCQLYTDPPEQSYTTITVLVPPRNLMIDIQKDTAVEG 141
Db 258 ISFNEDKSEMTIYRVEKDEAEYSC-IANNQAGEAEIIVLKVYAKPKMTYVKNKTVEL 316
QY 142 EEIENVCTAMASKPATITIRWFKGNKELKKGSEVSEWSDMYTWT-----SQMLKVKHED 195
Db 317 DEITLTCEA-SCDPIPSITWRTAHRNI---SSEKTLDGHIWVKDHIRMSALTLDIQYT 372
QY 196 DGVPIQVQHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTRFGDAPFELTCEATGKP 255
Db 373 DAGEYFCVASNP-IGVDQAM-YFEVQYAPKIR---GPVVVYWEQNPVNTCDVLAHP 426
QY 256 QPVMVTVVRVDEMPQH-----AVLSGP---NLFNNLNKTDNGTYRCEASNVGKAHSD 307
Db 427 S-AAVSWFRDQLLPSSNFSNFKIYNGTFFSLEVPDSEDFGNYNCASVNSIGHESSE 485
QY 308 YMLVYDPTPIPPPTTIRAG 346
Db 486 FILVQADTPSS---PAIRKVPYPSVTVMVEFDEPDATGG 521
RESULT 15
NPNH MOUSE
ID NPNH MOUSE STANDARD; PRT; 1242 AA.
AC Q9QZS7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nephlin precursor (Renal glomerulus-specific cell adhesion receptor).
GN NPHS1 OR NPHN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.
RX MEDLINE=99436348; PubMed=10504499;
RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holthofer H.,
RA Abrahamson D.R.;
RT "Nephlin localizes to the slit pore of the glomerular epithelial
RT cell.";
RL Kidney Int. 56:1481-1491(1999).
RN [2]
RP INTERACTION WITH CD2AP.
RX MEDLINE=21590051; PubMed=11733379;
RA Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
RA "CD2AP localizes to the slit diaphragm and binds to nephrin via a
RT novel C-terminal domain.";
RL Am. J. Pathol. 159:2303-2308(2001).
RN [3]
RP INTERACTION WITH CD2AP AND NPHS2.
RX MEDLINE=21590460; PubMed=11733557;
RA Schwarz K., Simons M., Reiser J., Saleem M.A., Paul C., Kriz W.,
RA Shaw A.S., Holzman L.B., Mundel P.;
RT "Podocin, a raft-associated component of the glomerular slit
RT diaphragm, interacts with CD2AP and nephrin.";
RL J. Clin. Invest. 108:1621-1629(2001).
CC -!- FUNCTION: Seems to play a role in the development or function of
CC the kidney glomerular filtration barrier. May anchor the podocyte
CC slit diaphragm to the actin cytoskeleton.
CC -!- SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
CC domain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
CC at podocyte slit diaphragm between podocyte foot processes.
CC -!- TISSUE SPECIFICITY: Expressed in kidney glomeruli.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 8 immunoglobulin-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF168466; AAF03368.1; -.
CC MGD; MGI:1859637; Nphsl.
CC GO; GO:0005515; P:Protein binding; IPI.
CC GO; GO:0007254; P:JNK cascade; IDA.
CC GO; GO:0000165; P:MAPKK cascade; IDA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; IG_c2.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00047; ig; 8.
CC SMART; SM00060; FN3; 1.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG LIKE; 8.
KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Phosphorylation.
FT SIGNAL 1 22
FT CHAIN 23 1242
FT DOMAIN 23 1064
FT TRANSMEM 1065 1086
FT DOMAIN 1087 1242
FT DOMAIN 1243 130
FT IG-LIKE C2-TYPE 1.

QY	184	-TSQLMLKVKHKDDGVPVICQVEHPAVTGNLQTORYLEVQVKPQVHIOMTYPLQGLITREG	242
Dd	262	SNTLTVRNIINSOGPVVCRTATKA--GEDEKQAFLOVFQPHI-IQLK---NETTYEN	315
QY	243	DAFELTCCEAIGKPQVMVTWR-VD-----DEMP-----OHAVLGSNGPNLFNNLN	286
Dd	316	GQVTLVCDAAEGEPIP-EITWKRAVDGFTTFTEGDKSPDGRIEVKGQH---GSSSLHKKDKV	371
QY	287	KTDNGTVRCE-ASNVGKAHSYDMLYVY-----DPPPTT	318
Dd	372	LSSGRGYDCEAASRIGGHQSMYLDIEYAPKFISNQTIYSWEGNPNINISCDVKNPPAS	431
QY	319	I-----PPPTTTTTTTTTTTILTIITDSRAGEEGTIGADVHAVIGGVAVVVPA	369
Dd	432	IHWFRDKLVLPAKTNLTKVSTGRKMILELAPTSDNDFGVNCATATHIGTRFOEYILA	491
QY	370	MLCL-----LIILGRYFAR-----HGKYVFFTHEAKGADDAADATAINAEGGO	413
Dd	492	LADVPSPYPYGKIIELSOTTAQVSFNKPDShGGVPIHHIVQDVVKVEASEIWKLIVSHGVQ	551
QY	414	-----NNSEKKEY	422
Dd	552	TWVVLNNLEPNTTY	565

RESULT 14

ID	NC_A2_XENLA	STANDARD;	PRT; 1092 AA.
AC	P36335;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM 180).		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
ON	NCBI_TaxID=8355;		
OR	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93273239; PubMed=7684721;		
RT	Tonissen K.F., Krieg P.A.;		
FA	"Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are expressed during development and in adult tissues.";		
RL	Gene 127:243-247(1993).		
CC	-/- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc.		
CC	-/- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-/- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=1;		
CC	Comment=A number of isoforms are produced;		
CC	Name=1;		
CC	Isoid=P36335-1; Sequence=Displayed;		
CC	-/- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.		
CC	-/- SIMILARITY: Contains 2 fibronectin type III domains.		

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DR	EMBL; M76710; AAA49910.1; --
DR	PIR; JN0635; JN0635.
DR	HSSP; P56276; ITLK.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR003961; FN_III.


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FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT GPI-ANCHOR 321 321 GPI-ANCHOR AMIDATED ASPARAGINE
FT LIPID 321 321 (POTENTIAL).
SQ SEQUENCE 344 AA; 37998 MW; CBB39B5E3H3B224 CRC64;

Query Match 10.5%; Score 231; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 1.5e-09;
Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY 10 LLLLLLSAALIPG-----DQNLFTK---DVTVIEGEVATISQVNVKSDSVIQLNPN 62
Db 14 LVVSLRLFLVPTGVPVRSQDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN 70
QY 63 RQTI-YFRDFRPLKDSRFQLLNFSSSELKVSLSNVISDEGRYFCQLYTD-PPQESYTTI 120
Db 71 RSTILYAGNDKWCLDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSRVHL 130
QY 121 TVLVPPRLMIDIKQTA-V-EGEIEVNCVTAMASKPATIRWFKGNKELGKSEVEWSD 179
Db 131 IVQVSPK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGFVSEDEYLE 187
QY 180 MYTVTSQMLKVH---KEDDGVPIQVEHPAVTGNLQRTQRYLEVQYKPOVHIQMTYPLQ 236
Db 188 IQGTRQSGDYECASNDVAAPVVRV-----VTNYPYIS-----EAK 229
QY 237 GL-TREGDAFELTCEATGKQFQVMTVVRVDEMPQ-----HAVLSGPNLFINLN 286
Db 230 GTGVPVQKGTQCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLRLTF--NVS 286
QY 287 KTDNGTYRCEASNIIVGKAHSDYMLY 311
Db 287 EHDYGNVTCVASKLGHNTASIMLF 311

RESULT 11
NTRI HUMAN
ID NTRI HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hNT).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR DR MIM; 607938; -.
DR GO; GO:008038; P:neuronal cell recognition; TAS.
```

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00835; Ig_Like; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT CHAIN 1 31 POTENTIAL.
FT SIGNAL 31 31 NEUTROTRIMIN.
FT PROPEP 32 344 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-ANCHOR AMIDATED ASPARAGINE
SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;

Query Match 10.4%; Score 229; DB 1; Length 344;
Best Local Similarity 26.3%; Pred. No. 2.1e-09;
Matches 85; Conservative 57; Mismatches 135; Indels 46; Gaps 15;

QY 10 LLLLLLSAALIPG-----DQNLFTK---DVTVIEGEVATISQVNVKSDSVIQLNPN 62
Db 14 LVVSLRLFLVPTGVPVRSQDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN 70
QY 63 RQTI-YFRDFRPLKDSRFQLLNFSSSELKVSLSNVISDEGRYFCQLYTD-PPQESYTTI 120
Db 71 RSTILYAGNDKWCLDPRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSRVHL 130
QY 121 TVLVPPRLMIDIKQTA-V-EGEIEVNCVTAMASKPATIRWFKGNKELGKSEVEWSD 179
Db 131 IVQVSPK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGFVSEDEYLE 187
QY 180 MYTVTSQMLKVH---KEDDGVPIQVEHPAVTGNLQRTQRYLEVQYKPOVHIQMTYPLQ 236
Db 188 IQGTRQSGDYECASNDVAAPVVRV-----VTNYPYIS-----EAK 229
QY 237 GL-TREGDAFELTCEATGKQFQVMTVVRVDEMPQ-----AVLSGP---NLPINLNKT 288
Db 230 GTGVPVQKGTQCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLKLIFFNVSEH 288
QY 289 DNGTYRCEASNIIVGKAHSDYMLY 311
Db 289 DYGNVTCVASKLGHNTASIMLF 311

RESULT 12
NCM2 MOUSE
ID NCM2 MOUSE STANDARD; PRT; 837 AA.
AC Q35136; Q35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
```

Query Match 10.5%; Score 231.5; DB 1: Length 417;

Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L., Shannon M., Brower A., Olsen A.S., Smith L.M.; "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger gene cluster."; Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. [5]
 DOMAINS.
 MEDLINE=91239515; PubMed=18511992;
 Koike S., Ise I., Nomoto A.;
 "Functional domains of the poliovirus receptor."; Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991). [6]
 MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
 MEDLINE=93059689; PubMed=1331527;
 Zibert A., Wimmer E.;
 "N glycosylation of the virus binding domain is not essential for function of the human poliovirus receptor."; J. Virol. 66:7368-7373(1992).
 -1- FUNCTION: Not known. Used by poliovirus to bind and enter the cell.
 -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoforms beta and gamma).
 -1- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=4;
 Name=Alpha;
 IsoId=P15151-1; Sequence=Displayed;
 Name=Beta;
 IsoId=P15151-2; Sequence=VSP_002617;
 Name=Gamma;
 IsoId=P15151-3; Sequence=VSP_002618; VSP_002619;
 Name=Delta;
 IsoId=P15151-4; Sequence=VSP_002620; VSP_002621;
 MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR VIRUS BINDING AND UPTAKE.
 -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 -1- SIMILARITY:

ID	PVR_HUMAN	STANDARD;	PRT;	417 AA.
AC	F15151;	P15152; Q15267;	Q15268;	
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Poliovirus receptor precursor (CD155 antigen).			
DE	PVR OR PVS.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89168426; PubMed=2538245;			
RA	Mendelsohn C.L., Wimmer E., Racaniello V.R.;			
RT	"Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expression of a new member of the immunoglobulin superfamily.";			
RT	Cell 56:855-865(1989).			
RL	[2]			
RL	REVISONS.			
RA	Racaniello V.R.;			
RP	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RX	MEDLINE=91060615; PubMed=2170108;			
RA	Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,			
RA	Takeuchi K., Takesami T., Nomoto A.;			
RT	"The poliovirus receptor protein is produced both as membrane-bound and secreted forms.";			
RL	EMBO J. 9:3217-3224(1990).			
RL	[4]			
RP	SEQUENCE FROM N.A.			

```

KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1088
FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1088
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 209 294
FT DOMAIN 303 397
FT DOMAIN 400 484
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
FT VARSPLIC 804 1049
FT
SQ SEQUENCE 1088 AA; 117778 MW; 6273855B03F3E83 CRC64;

Query Match 10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 3.9e-09;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 32 KDVTVIEGEVATISC---QVKNK---DDSVQLN---PNQTIYFRDPLKDSRFL 81
DB 199 KDIQVNVNPTQARQLRVNATANAESVLSDCADGFPDPEISWLKGEPIEDGE-EK 257
QY 82 LNFSSSELKSLTVNVSIDSEGRYPCQLVTPQPSRYTTITVLVPRNLMDIQDITAVEG 141
DB 258 ISFNEDQSEMTIHVEXKDEAEYSC-TANNCAGAEATILLKVAKYKIYVENKTAVEL 316
QY 142 BEIEVNTAMASKPATIRWPKGNK-----LKGKSEVEESDMVTVSQMLKVHKE 194
DB 317 DEITLTCEA-SGDPIPSITWRTAVRNISSEATTLLDGHVVKHEIRM-----SALTLDKIY 371
QY 195 DGGVPVICQVEHPAVTGNLQTVLEYQYKPOVHIQMTYPLQGLTRGDAFELTCEALGK 254
DB 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR-----GPVVVVTWEGNPNVITCEVFAH 425
QY 255 PQPVMTVWRVDDMPQH-----AVLSGP---NLFINNKNLTDNGTYRCEASNIIVGKAHS 306
DB 426 PR-AAVTWFRDGLQLPSSNFENIKIYSGPTSSLEVNPDSNDFGNYNCTALNTIGHFS 484
QY 307 DYMLYVVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
DB 485 EFILVQADTPSS---PAIRKVEYSYSTMIVDFDPDSTGG 521

RESULT 8
NTRI_MOUSE STANDARD; PRT; 344 AA.
AC Q99PJ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

```

RN RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
 RT "Cloning and expression of mouse neurotrophin gene in the developing
 RL nervous system."; submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 FT human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL
 CC -!- FUNCTION: Neural cell adhesion molecule.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLN
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC
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 CC or send an email to license@isb-sib.ch.
 CC
 CC EMBL; AF282980; AA00276.1; -;
 CC EMBL; BC023307; AA023307.1; -;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003599; Ig_c2.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SMC0409; IG; 3.
 CC SMART; SMC0408; IGC2; 3.
 CC PROSITE; PS50835; IG LIKE; 3.
 CC Immunoglobulin domain; Cx11 adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Lipoprotein.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 321 NEUOTRIMIN.
 FT PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
 FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
 FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
 FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
 FT DISULFID 157 201 POTENTIAL.
 FT DISULFID 157 201 POTENTIAL.
 FT DISULFID 243 295 POTENTIAL.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 321 321 GPI-anchor amidated asparagine
 FT LIPID 321 321

RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
 RT "A second gene for the African green monkey poliovirus receptor that
 RT has no putative N-glycosylation site in the functional N-terminal
 RT immunoglobulin-like domain."
 RL J. Virol. 66:7059-7066(1992).
 CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
 CC cell.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
 CC Secreted (isoforms beta and gamma).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=Alpha;
 CC IsoId=P32506-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=P32506-3; Sequence=Not described;
 CC Name=Gamma;
 CC IsoId=P32506-4; Sequence=Not described;
 CC Name=Delta;
 CC IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;
 CC Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D12611; BAA02136.1; -;
 CC EMBL; D12612; BAA02137.1; -;
 CC PIR; A44194; A44194.
 CC PIR; B44194; B44194.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_v.
 CC Pfam; PF00047; Ig_3.
 CC SMART; SM00406; Ig; 1.
 CC PROSITE; PS00835; IG LIKE; 3.
 CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 417 POLIOVIRUS RECEPTOR.
 FT DOMAIN 21 343 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 344 367 POTENTIAL.
 FT DOMAIN 368 417 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 139 IG-LIKE V-TYPE.
 FT DOMAIN 145 237 IG-LIKE C2-TYPE 1.
 FT DOMAIN 244 328 IG-LIKE C2-TYPE 2.
 FT DISULFID 49 123 BY SIMILARITY.
 FT DISULFID 166 221 BY SIMILARITY.
 FT DISULFID 266 312 BY SIMILARITY.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
 FT FTid=VSP_002622.
 FT Missing (in isoform Delta).
 FT VARSPPLIC 393 417 /FTid=VSP_002623.
 FT FTid=VSP_002623.
 SQ SEQUENCE 417 AA; 45464 MW; DA4A0FE4D2F6E1F CRC64;
 Query Match 10.8%; Score 237; DB 1; Length 417;
 Best Local Similarity 23.8%; Pred. No. 7.1e-10;
 Matches 107; Conservative 68; Mismatches 194; Indels 80; Gaps 18;
 QY 1 AAPPGLRLRLLLLSAAALIPDTGGQNLTKDVTV--IEGEVATISC--QWNKSDSDSVI 56
 DB 8 AWPP-----LLLTLLLSWPPPGTGDIIQVAPTCVPGFLGDSVTLPCYLQVPGMEETHV 61

RESULT 6

PVR1_MOUSE
 ID PVR1_MOUSE STANDARD; PRT; 515 AA.
 AC Q9JKE6; Q9JEL5; Q9JIL7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
 DE mediator C) (HvEC) (Nectin 1).
 GN PVR1 OR PRR1 OR HVEC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20243787; PubMed=10781093;
 RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
 RA Lecoq E., Dubreuil P., Campadelli-Fiume G.;
 RT "The murine homolog of human nectin delta serves as a species
 RT nonspecific mediator for entry of human and animal alpha herpesviruses
 RT in a pathway independent of detectable binding to gp."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20541977; PubMed=11090177;
 RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
 RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha
 RT (HvEC) in sequence and activity as a glycoprotein D receptor for
 RT alphaherpesvirus entry."
 RL J. Virol. 74:11773-11781(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster;
 RA Zhan J., Wimmer E.;
 RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the
 RT floor plate during embryogenesis, suggesting a role in neural
 RT development."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
 CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
 CC CELLS.
 CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gp).
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.

QY 100 DEGRYFCOLYTDPR--POESYTTIVLPVPPNLMIDIQDTAVEGEELEV-----NCT 149
 Db 125 DEGNYTCFATFNGTRRGVTLWLRVIAQPN-----HAAEQEVTIGPSVAVARCV 175
 QY 150 AMASKPATITRPFKG-NKELKGKSEVEWSDMYVTLSQLMKVHKEDDGVPIQVEHPA 208
 Db 176 STGRRPARITWISSLGGEAKDTQEPGIQAGVTIIISYSLVPVGRADGVKVTCKVEHS 235
 QY 209 VTGNLQTORVLEVOYKPVQVHIQMTYPLQGTREGDAFELTCEAIGKQPQVMVTWVRVDD 268
 Db 236 FEBPILLPVTLVSRYPPEVSI-GYDDNWYLGRSEAI-LTCDVRESNEPTDYDWSITSGV 293
 QY 269 MPQHAVLSGNLFINLNKNTDNGTYRCEASNIYGVKASHDMLYVDPTTIPPTTTTT 328
 Db 294 FPAVAQGSQLLVHSDVMNTFFICTATNAVGTGRAQVILVRESFST----- 343
 QY 329 TTTTITITITIDSRAGEEGTICAVDHVIGGVAVVW 367
 Db 344 -----AGATGG-----TIGGIIAII 361

RESULT 4

PVR2 HUMAN

ID PVR2 HUMAN STANDARD; PRT; 538 AA.

AC Q92692: O75455: Q96J29;

DT 16-OCT-2001 (Rel. 40, Created)

DT 18-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HvEB) (Nectin 2) (CD112 antigen).

GN PVR2 OR PRR2 OR HVEB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI_TaxID=9606;

RX [1]

RP SEQUENCE FROM N.A. (ISOFORM DELTA).

RX MEDLINE=95347610; PubMed=7622062;

RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;

RT "The human PRR2 gene, related to the human poliovirus receptor gene

RT (PVR), is the true homolog of the murine MPH gene.";

RL Gene 159:267-272(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RX MEDLINE=98321161; PubMed=9657005;

RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,

RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;

RT "A cell surface protein with herpesvirus entry activity (HvEB) confers

RT susceptibility to infection by mutants of herpes simplex virus type

RT 1, herpes simplex virus type 2, and pseudorabies virus.";

RL Virology 246:179-189(1998).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey C., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko J.W., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,

RA Scherch A., Schein J.E., Jones S.T.M., Warren W.A.

[illegible]

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FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB0032DDDE3785 CRC64;

Query Match 11.8%; Score 259.5; DB 1; Length 515;
Best Local Similarity 24.5%; Pred. No. 2.2e-11;
Matches 107; Conservative 61; Mismatches 165; Indels 103; Gaps 18;

QY 34 VTVIEGEVATISQCNKSDSDSVIQLNPNRTIYFRDPRFLKDSRFQLNFSSELKVS 93
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 ITQVTKATNGSKQN-----VAIYNPAMGVSVLAPYR-----ERVEFLRPSFTDGTIRL 111
QY 94 TNVTSIDSGRYFCQLYTDP--QSYTITVLVPRNLMIDIQ-----KDTAVEGER 143
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 SRLEDEGVICFATPPAGNRSQNLTVAKPTNWIETQAVLRKAGKDDKVV----- 167
QY 144 IEVNCTAMASKPATIRFKGNKELKSKSEVEW---SDMTVTVSQMLKVHKEDDGVVP 200
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
168 LVATCTSANGKPPSVSW--ETHLKGAEEVQELRNPNGTVTVISRYLVPSPRDRHQSL 224
QY 201 ICQVEHPAVTNLQTRY-----LEVQKPOVHIQ---MTVPLQGLTRGDAFELTCEAI 252
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
225 ACIV-----NYHMDRFRESLTINVQEPVETIEGFGNWLQRM-----VKLTCKAD 272
QY 253 GKQPQVMVTVRVDMPQHAVLSQNLFINN-LNKTDNGTYRCEASNIYKASHDYM 311
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
273 ANPATEYHTWTLNGLSLPKGVEAQNTLFFRGPINYSWAGTYICEATNPICTRSGQVEVN 332
QY 312 VYDPPTTPIPTTTTTTTTTTTTTTTTTTTTTTILATITDSRAGEEG-TIGAVDHAIVIGGWA---VVV 367
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
333 ITEPPTPSP--E-----EHGRRAGQVPTAIGVGVSILLVL 368
QY 368 FAMLCLLIILGRYPARKGTFT-----HEAKGA-----DDAADATA 405
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
369 FVGGIVVALCRRHRTFKGDYSTKHHVYNGSYKAGIPQHHPPMAQNLQYEPEDSDDEKKA 428
QY 406 IINAEAGGONNSEEKKE 421
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
429 --GLPGSSYEEREE 442

```

RESULT 2

```

PVRI HUMAN STANDARD; PRT; 517 AA.
AC Q1523; Q75465; Q9HBE6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (Higr) (CD111 antigen).
DE PVRL1 OR PVRL1 OR HVEC.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabart J., Bardin F., Maroc C., Dubreuil P.;
RT "CDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene.";

```

```

Gene 155:261-265(1995).
[2]
SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE=98279152; PubMed=9616127;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
Spear P.G.;
"Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";
Science 280:1618-1620(1998).
[3]
SEQUENCE FROM N.A. (ISOFORM GAMMA).
MEDLINE=21256041; PubMed=11356977;
Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.;
"Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin (or prr1-Hgr-HvEC) modulates positively and negatively susceptibility to hsv infection.";
J. Virol. 75:5684-5691(2001).
[4]
SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
MEDLINE=2032396; PubMed=10932188;
Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
"Mutations of PVRL1, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal dysplasia.";
Nat. Genet. 25:427-430(2000).
-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=Delta;
IsoId=Q15223-1; Sequence=Displayed;
Name=Alpha;
IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
Name=Gamma;
IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
-!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is responsible for allelic forms known as Margarita island ectodermal dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930.g.htm".
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-----
EMBL; X76400; CAA53980.2; ALT_INIT.
EMBL; AF060231; AAC23798.1; -.
EMBL; AY029539; AAK3124.1; -.
EMBL; AF252867; AAG16648.1; -.
EMBL; AF196768; AAG16648.1; JOINED.
EMBL; AF196769; AAG16648.1; JOINED.
EMBL; AF196770; AAG16648.1; JOINED.
EMBL; AF196771; AAG16648.1; JOINED.
EMBL; AF196774; AAG16649.1; -.
EMBL; AF196768; AAG16649.1; JOINED.
EMBL; AF196769; AAG16649.1; JOINED.
EMBL; AF196770; AAG16649.1; JOINED.
EMBL; AF196771; AAG16649.1; JOINED.
EMBL; AF196772; AAG16649.1; JOINED.
EMBL; AF196773; AAG16649.1; JOINED.

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 8.98407 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187b-4

Perfect score: 2197

Sequence: 1 AAPPGRLRLRLLLLSAAL.....TAINAEGGQNGNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259.5	11.8	515	1 PVR1_PIG	Q9GL76 sus scrofa
2	252.5	11.5	517	1 PVR1_HUMAN	P15223 homo sapien
3	243	11.1	530	1 PVR2_MOUSE	Q12507 mus musculus
4	238.5	10.9	538	1 PVR2_HUMAN	Q92692 homo sapien
5	237	10.8	417	1 PVR_CERAB	P32506 cercopithec
6	236	10.7	515	1 PVR1_MOUSE	Q9JKE6 mus musculus
7	234	10.7	1088	1 NCAL_XENLA	P16170 xenopus lae
8	232	10.6	344	1 NTRI_MOUSE	Q99PJ0 mus musculus
9	231.5	10.5	417	1 PVR_HUMAN	P15851 homo sapien
10	231	10.5	344	1 NTRI_RAT	Q62718 rattus norv
11	229	10.4	344	1 NTRI_HUMAN	Q9P121 homo sapien
12	225.5	10.3	837	1 NCM2_MOUSE	O35136 mus musculus
13	222	10.1	837	1 NCM2_HUMAN	O15394 homo sapien
14	222	10.1	1092	1 NCA2_XENLA	P36335 xenopus lae
15	221	10.1	1242	1 NPHN_MOUSE	Q9QZ67 mus musculus
16	220.5	10.0	338	1 LAMP_MOUSE	Q98919 gallus gall
17	220	10.0	337	1 OPMC_CHICK	Q98992 gallus gall
18	218	9.9	563	1 C166_MOUSE	P61490 mus taurus
19	217.5	9.9	345	1 OPMC_BOVIN	P11834 bos taurus
20	215.5	9.8	345	1 OPMC_HUMAN	Q14982 homo sapien
21	214	9.7	588	1 C166_CHICK	P42292 gallus gall
22	211	9.6	847	1 CD22_HUMAN	P20273 homo sapien
23	211	9.6	4391	1 PGBM_HUMAN	P98160 homo sapien
24	209.5	9.5	345	1 OPMC_RAT	P32736 rattus norv
25	209	9.5	353	1 CEPU_CHICK	Q90773 gallus gall
26	207.5	9.4	509	1 SHS1_RAT	P97710 x protein-t
27	207.5	9.4	646	1 MUI8_HUMAN	P43121 homo sapien
28	207	9.4	1493	1 NEOL_MOUSE	P97798 mus musculus
29	206.5	9.4	338	1 NEOL_HUMAN	Q13449 homo sapien
30	206.5	9.4	862	1 CD22_MOUSE	P35329 mus musculus
31	204.5	9.3	338	1 LAMP_RAT	Q62813 rattus norv
32	204	9.3	702	1 CEAS_HUMAN	P06731 homo sapien
33	203.5	9.3	583	1 C166_HUMAN	Q13740 homo sapien

34	203	9.2	1461	1 NEOL_HUMAN	Q2859 homo sapien
35	202	9.2	1443	1 NEOL_CHICK	Q90610 gallus gall
36	198	9.0	1377	1 NEOL_RAT	P97603 rattus norv
37	197	9.0	3707	1 PGBM_MOUSE	Q05793 mus musculus
38	196.5	8.9	1241	1 NPHN_HUMAN	O60500 homo sapien
39	196.5	8.9	1331	1 CTA2_HUMAN	Q9H0C6 homo sapien
40	195	8.9	506	1 SHS1_BOVIN	O46631 bos taurus
41	194	8.8	1091	1 NCA1_CHICK	P13590 gallus gall
42	193	8.8	761	1 NCA2_HUMAN	P13592 homo sapien
43	193	8.8	848	1 NCA1_HUMAN	P13591 homo sapien
44	192.5	8.8	1036	1 AXO1_CHICK	P28685 gallus gall
45	191.5	8.7	853	1 NCA1_BOVIN	P31836 bos taurus

ALIGNMENTS

RESULT 1

PVR1_PIG STANDARD; PRT; 515 AA.

AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
DE mediator C) (HveC) (Nectin 1).
GN PVR1L OR PVR1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family, is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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EMBL; AF308632; AAG30281.1; --
DR HSSP; P06907; 1NEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLU.

APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 48.5%; Score 1012.5; DB 2; Length 444;
Best Local Similarity 48.7%; Pred. No. 6.2e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGGVVLKQVQKDHEDSLQWSPAAQOTLYFGEKRALDRNRIQLVSTPHE 92
Db 36 PLTONVTVVGGTALTCTCRVDQNDNTSLQWSPAAQOTLYFDDKKALDRNRIELVRASWHE 95
QY 93 LSTISNVALADEGYTCSIFTMVPTAKSLVTLVGIPOKPIITGYKSLREKDTATLNC 152
Db 96 LSTISVSDVSLDEGQYTCSLFTMPVKTAKSLVTLVGIPOKPIITGYKSLREKDTATLNC 155
QY 153 QSSGSKPAARLTWRKQDQELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSYN 212
Db 156 KTSGSKPAADIRWFKNDRKIKDVYKLBEDANRKTFTVSSSTLDFRVDSDGVAVICRDV 215
QY 213 HESLKGADRTSQRILEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPVPOYLWEKES 272
Db 216 HESLNATPQVAMQVLEIHTVPSVKIIPSTPFQEGQPLITCESKGLPEPVLWKDGG 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTCTATSNMGSKAYVTLNVND-----PSPV- 322
Db 276 ELPPDRMVVSGRELNLFLNKTNDCTYCEATNTIGQSAEYVLIVHVDVNTLPTTII 335
QY 323 -----PSSSTY-----HAIIGIVAFIVFLLLIMI 349
Db 336 PSLTATVTTTVAITTSPTTSATTSIRDPNALAGQPDHALIGGIVAVVVFVTLCSIF 395
QY 350 FLGHYLIRHGYLTHEAGSDADPADATAIINAEQSGGDDKKEYFI 398
Db 396 LLGRYLARHKGTYLNEAGGADPADATAIINAEQSQVNAEKKEYFI 444

RESULT 11

US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 48.5%; Score 1012.5; DB 3; Length 444;
Best Local Similarity 48.7%; Pred. No. 6.2e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGGVVLKQVQKDHEDSLQWSPAAQOTLYFGEKRALDRNRIQLVSTPHE 92
Db 36 PLTONVTVVGGTALTCTCRVDQNDNTSLQWSPAAQOTLYFDDKKALDRNRIELVRASWHE 95
QY 93 LSTISNVALADEGYTCSIFTMVPTAKSLVTLVGIPOKPIITGYKSLREKDTATLNC 152
Db 96 LSTISVSDVSLDEGQYTCSLFTMPVKTAKSLVTLVGIPOKPIITGYKSLREKDTATLNC 155
QY 153 QSSGSKPAARLTWRKQDQELHCEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSYN 212
Db 156 KTSGSKPAADIRWFKNDRKIKDVYKLBEDANRKTFTVSSSTLDFRVDSDGVAVICRDV 215
QY 213 HESLKGADRTSQRILEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPVPOYLWEKES 272
Db 216 HESLNATPQVAMQVLEIHTVPSVKIIPSTPFQEGQPLITCESKGLPEPVLWKDGG 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTCTATSNMGSKAYVTLNVND-----PSPV- 322
Db 276 ELPPDRMVVSGRELNLFLNKTNDCTYCEATNTIGQSAEYVLIVHVDVNTLPTTII 335
QY 323 -----PSSSTY-----HAIIGIVAFIVFLLLIMI 349
Db 336 PSLTATVTTTVAITTSPTTSATTSIRDPNALAGQPDHALIGGIVAVVVFVTLCSIF 395

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/659,984A
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,152
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002810US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-659-984A-1

Query Match 48.5%; Score 1012.5; DB 2; Length 421;
 Best Local Similarity 48.7%; Pred. No. 5.7e-84;
 Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
 QY 33 PWTSDTEVAGGTVVLKCOVKDHEDSSLOWSPNAQOTLYFGEKRALDNRILQVTSPTPHE 92
 DB 13 PLTONVTVVEGGTAITLCRVQDNDNTSLOWSPNAQOTLYFDDKKALDRNRIELVRASWHE 72
 QY 93 LSIISINVALADEGEYTCSTFTMPVTKSLVTVLGIPOKPIITGYKSSLRKDTATLNC 152
 DB 73 LSIISVDSVLSDEGQYTCSTFTMPVTKSKAYLTVLGVPEKPOISGSPSPWMEGDLMLQTC 132
 QY 153 QSGSKPAALRWKQDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGASIVCSVN 212
 DB 133 KTSKSPADIRWFKNDKEIKVKYLKEEDANRKTFTVSTLDFRDRSDGVAVICRVD 192
 QY 213 HESLKGADRTSQRILEVLYTPTAMIRPDPPHREGKLLHCEGRNVPVQOYLWEKGS 272
 DB 193 HESLNATPQVAMQVLEIHYTPSVKLIPTSTFPQEGQPLILTCESKGKPLPEPVLWTKDGG 252
 QY 273 V---PLKMTQESALIPFFLNKSDSGTYGCTATSNMGSYKAYITLVND-----PSPV- 322
 DB 253 ELPPDRMVVSGRELNLFLNKTNGHYRCEANTTIGQSSAEYVLIVHDVPTLLPTTII 312
 QY 323 -----PSSSTY-----HAIGGIVAFIVFLLIMLI 349
 DB 313 PSITATVTTTVAITTSPTTSATTSIRDPNALAGQNGPDHALIGGIVAVVFWTLCISIF 372
 QY 350 FLGHYLIRHKGYLTAEKSGDDAPADATAIINAEQSGGDDKKEYFI 398
 DB 373 LLGRYLARHKGYLTAEKGAEDAPADATAIINAEQSQVNAEKKEYFI 421

RESULT 9

US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Query Match 48.5%; Score 1012.5; DB 3; Length 421;
 Best Local Similarity 48.7%; Pred. No. 5.7e-84;
 Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
 QY 33 PWTSDTEVAGGTVVLKCOVKDHEDSSLOWSPNAQOTLYFGEKRALDNRILQVTSPTPHE 92
 DB 13 PLTONVTVVEGGTAITLCRVQDNDNTSLOWSPNAQOTLYFDDKKALDRNRIELVRASWHE 72
 QY 93 LSIISINVALADEGEYTCSTFTMPVTKSLVTVLGIPOKPIITGYKSSLRKDTATLNC 152
 DB 73 LSIISVDSVLSDEGQYTCSTFTMPVTKSKAYLTVLGVPEKPOISGSPSPWMEGDLMLQTC 132
 QY 153 QSGSKPAALRWKQDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGASIVCSVN 212
 DB 133 KTSKSPADIRWFKNDKEIKVKYLKEEDANRKTFTVSTLDFRDRSDGVAVICRVD 192
 QY 213 HESLKGADRTSQRILEVLYTPTAMIRPDPPHREGKLLHCEGRNVPVQOYLWEKGS 272
 DB 193 HESLNATPQVAMQVLEIHYTPSVKLIPTSTFPQEGQPLILTCESKGKPLPEPVLWTKDGG 252
 QY 273 V---PLKMTQESALIPFFLNKSDSGTYGCTATSNMGSYKAYITLVND-----PSPV- 322
 DB 253 ELPPDRMVVSGRELNLFLNKTNGHYRCEANTTIGQSSAEYVLIVHDVPTLLPTTII 312
 QY 323 -----PSSSTY-----HAIGGIVAFIVFLLIMLI 349
 DB 313 PSITATVTTTVAITTSPTTSATTSIRDPNALAGQNGPDHALIGGIVAVVFWTLCISIF 372
 QY 350 FLGHYLIRHKGYLTAEKSGDDAPADATAIINAEQSGGDDKKEYFI 398
 DB 373 LLGRYLARHKGYLTAEKGAEDAPADATAIINAEQSQVNAEKKEYFI 421

RESULT 10

US-08-659-984A-5
 ; Sequence 5, Application US/08659984A
 ; Patent No. 5942400
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Sinha, Sukanto

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Db 301 ATSNWGYTAFTLVNDPSPVSSSTYHAIIGGVAFIVFLDLLILLIFLGHYLIHKG 360
QY 361 TYLTAEKSGDDAPDAITAIIAEGGSGGDDKKEYEI 398
Db 361 TYLTAEKSGDDAPDAITAIIAEGGSGGDDKKEYEI 398

RESULT 7
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917

Query Match 57.0%; Score 1189; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.8e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ELSISISNVALADEGEYTCISFTMPVRTAKSLVTLVIGIPKPIITGYKSLREKDTATLN 151
Db 1 ELSISISNVALADEGEYTCISFTMPVRTAKSLVTLVIGIPKPIITGYKSLREKDTATLN 60
QY 152 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGASIVCSV 211
Db 61 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGASIVCSV 120
QY 212 NHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGEGNVPQOYLWEKEG 271
Db 121 NHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGEGNVPQOYLWEKEG 180
QY 272 SVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVND 318
Db 181 SVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVND 227

RESULT 8
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6.1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLLLLLLFACCAWPGGANLSQDDSQPWTSDTETVAGTIVLKCQVKHEDSSL 60
Db 1 MGAPASLLLLLLFACCAWPGGANLSQDDSQPWTSDTETVAGTIVLKCQVKHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
QY 361 TYLTAEKGSDDAPDADTAIINAEKGSQGGDDKKEYFI 398
Db 361 TYLTAEKGSDDAPDADTAIINAEKGSQGGDDKKEYFI 398

RESULT 5
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match      98.7%; Score 2059; DB 4; Length 432;
Best Local Similarity 92.1%; Pred. No. 2e-179;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPASLLLLLLFACCAWPGGANLSQDGYQEQDLELGTAPLDEALISSTVSSPDL 60
Db 1 MGAPASLLLLLLFACCAWPGGANLSQDGYQEQDLELGTAPLDEALISSTVSSPDL 60
QY 30 ----SQPWTSDTETVAGTIVLKCQVKHEDSSLQWSNPAQOTLYFGEKRALRDNRIQLV 86
Db 61 ASQDSQPWTSDTETVAGTIVLKCQVKHEDSSLQWSNPAQOTLYFGEKRALRDNRIQLV 120

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6.1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLLLLLLFACCAWPGGANLSQDDSQPWTSDTETVAGTIVLKCQVKHEDSSL 60
Db 1 MGAPASLLLLLLFACCAWPGGANLSQDDSQPWTSDTETVAGTIVLKCQVKHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
QY 361 TYLTAEKGSDDAPDADTAIINAEKGSQGGDDKKEYFI 398
Db 361 TYLTAEKGSDDAPDADTAIINAEKGSQGGDDKKEYFI 398

RESULT 6
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match      95.0%; Score 1982; DB 4; Length 398;
Best Local Similarity 95.0%; Pred. No. 1.9e-172;
Matches 378; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

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QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLTYPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNPVPQOVLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905/125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-84

Query Match 100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MGAPAAALLLLLLLACCCWAPGAGNLSDQSPWTSDETVVAGGTVVLKCOVKHEDSSL	60
QY	61	QWSNPAQOTLYGEGKRALRDNRIQLVTSPPHLSISISNVALADEGEYTCSTFTMPVATA	120
DB	61	QWSNPAQOTLYGEGKRALRDNRIQLVTSPPHLSISISNVALADEGEYTCSTFTMPVATA	120
QY	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSPKALRWKGDQELHGEPTRIQ	180
DB	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSPKALRWKGDQELHGEPTRIQ	180
QY	181	EDPNGKTTVSSSVTFQVTRDDGASIVCSNVHESLKGADRSSTORIEVLVYPTAMIRPD	240
DB	181	EDPNGKTTVSSSVTFQVTRDDGASIVCSNVHESLKGADRSSTORIEVLVYPTAMIRPD	240
QY	241	PHHPREGOKLLHCEGRGNVPVQQLWKEGSPVPLKMTQESALIFPFLNKSDSGTGCT	300
DB	241	PHHPREGOKLLHCEGRGNVPVQQLWKEGSPVPLKMTQESALIFPFLNKSDSGTGCT	300
QY	301	ATSNMGSKAYTYLNVNDPSPVPSSTVTHAIGGIVAFIVFLIMLIFLGHVLIIRHG	360
DB	301	ATSNMGSKAYTYLNVNDPSPVPSSTVTHAIGGIVAFIVFLIMLIFLGHVLIIRHG	360
QY	361	TYLTHEAKGSDADPADTATINAEQGSGDDKKEYFI	398

Db 361 TYLTHEAKGSDADPADTATINAEQGSGDDKKEYFI 398
RESULT 4
US-09-902-775A-84
Sequence 84, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 14.5581 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086
Sequence: 1 MGAPAAALLLLLLFACW.....AIINAEQSGGDKKEYFI 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/prodata/2/iaa/6A_COMB.pap.*
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6: /cgn2_6/prodata/2/iaa/backfile1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2086	100.0	398	4	US-09-778-510-6
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25	2086	100.0	398	4	US-09-778-510-6
26	2086	100.0	398	4	US-09-778-510-6
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28	228	10.9	338	2	US-08-414-657D-60	Sequence 60, Appl
29	228	10.9	338	4	US-09-135-080-8	Sequence 8, Appl
30	225.5	10.8	338	2	US-08-414-657D-42	Sequence 42, Appl
31	225.5	10.8	338	2	US-08-414-657D-43	Sequence 43, Appl
32	225.5	10.8	338	4	US-09-135-080-4	Sequence 4, Appl
33	225	10.8	338	4	US-09-976-594-404	Sequence 404, App
34	224.5	10.8	582	4	US-09-702-705-334	Sequence 334, App
35	224.5	10.8	582	4	US-09-736-457-334	Sequence 334, App
36	224.5	10.8	582	4	US-09-614-124B-334	Sequence 334, App
37	224.5	10.8	582	4	US-09-671-325-334	Sequence 334, App
38	224.5	10.8	582	4	US-09-589-184-334	Sequence 334, App
39	223.5	10.7	583	2	US-08-432-016-2	Sequence 2, Appl
40	223.5	10.7	583	2	US-08-684-594-2	Sequence 2, Appl
41	222	10.6	315	2	US-08-414-657D-47	Sequence 47, Appl
42	221.5	10.6	518	4	US-09-919-172-20	Sequence 20, Appl
43	221.5	10.6	698	2	US-08-602-725-36	Sequence 36, Appl
44	221.5	10.6	734	2	US-08-389-459A-17	Sequence 17, Appl
45	221.5	10.6	734	3	US-08-987-867A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:

; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

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Best Local Similarity						100.0%; Pred. No. 6.1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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QY	61	QWSNPAQOTLYEGERALDRNRQLVTPHLSISINVALADEGYTCSTFTMPVTA	120			
Db	61	QWSNPAQOTLYEGERALDRNRQLVTPHLSISINVALADEGYTCSTFTMPVTA	120			
QY	121	KSLVTVLGPQPIITGVKSSIREKDTATLNCQSSGSKPAARLTWRKQDHLGEPTRIQ	180			
Db	121	KSLVTVLGPQPIITGVKSSIREKDTATLNCQSSGSKPAARLTWRKQDHLGEPTRIQ	180			
QY	181	EDPNKGTFTVSSSVTFQVTRDDGASIVCSNVHSLKADRSQRIEVLVYPTAMIRPD	240			
Db	181	EDPNKGTFTVSSSVTFQVTRDDGASIVCSNVHSLKADRSQRIEVLVYPTAMIRPD	240			
QY	241	PHHPREGKLLHLCGRGNVPVQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT	300			
Db	241	PHHPREGKLLHLCGRGNVPVQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT	300			
QY	301	ATSNMGSKAYTYLNVNDPSPVPSSTSYTHAIGIVAFIVFLLLIMLIFLGHYLRHKG	360			
Db	301	ATSNMGSKAYTYLNVNDPSPVPSSTSYTHAIGIVAFIVFLLLIMLIFLGHYLRHKG	360			

Thu May 27 10:42:50 2004

us-09-778-187b-10.rapb

Page 12

Job time : 34.8124 secs

Query Match 100.0%; Score 2086; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGAPAAALLLLLFACCCWAGGANLSQDDSQPWTSDTIVAGGTIVLKQVQKHEDSSL 60

QY 61 QMSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCISFTMPVRTA 120
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QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKQDELHGEPTRIQ 180
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QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADSTQRIEVLVYPTAMIRPD 240
DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADSTQRIEVLVYPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNPVPQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGQKLLHCEGRGNPVPQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT 300

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QY 361 TYLTHEAGSDDAPADTAINAEGGSGGDDKKEYFI 398
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RESULT 15

US-09-904-859-84
Sequence 84, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PFT
ORGANISM: Homo Sapien
US-09-904-859-84

Query Match 100.0%; Score 2086; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAALLLLLFACCCWAGGANLSQDDSQPWTSDTIVAGGTIVLKQVQKHEDSSL 60
DB 1 MGAPAAALLLLLFACCCWAGGANLSQDDSQPWTSDTIVAGGTIVLKQVQKHEDSSL 60

QY 61 QMSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCISFTMPVRTA 120
DB 61 QMSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCISFTMPVRTA 120

QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKQDELHGEPTRIQ 180
DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKQDELHGEPTRIQ 180

QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADSTQRIEVLVYPTAMIRPD 240
DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADSTQRIEVLVYPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNPVPQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGQKLLHCEGRGNPVPQQLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYITLVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIHRKG 360
DB 301 ATSNMGSKAYITLVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIHRKG 360

QY 361 TYLTHEAGSDDAPADTAINAEGGSGGDDKKEYFI 398
DB 361 TYLTHEAGSDDAPADTAINAEGGSGGDDKKEYFI 398

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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-84

```

```

Query Match      100.0%; Score 2086; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAALLLLLLFACCPAGGANTSDPSQDTSDETVVAGTVVVKQVXDHEDSSL 60
Db 1 MGAPAAALLLLLLFACCPAGGANTSDPSQDTSDETVVAGTVVVKQVXDHEDSSL 60

QY 61 QWNPAAQOTLYFGKRALRDNRIQLVTSSTPELSISISNVALADEGYTCISFTMPVRTA 120
Db 61 QWNPAAQOTLYFGKRALRDNRIQLVTSSTPELSISISNVALADEGYTCISFTMPVRTA 120

QY 121 KSLVTVLGIPQKPIITGYKSLREKOTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKOTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180

QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYTTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYTTAMIRPD 240

QY 241 PPHREGQKLLHCEGKGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGKGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSYKAYYTLNNDPSPVSSSTYHAIIGGIVAFIVFLLMLFLGHYLRHKG 360
Db 301 ATSNMGSYKAYYTLNNDPSPVSSSTYHAIIGGIVAFIVFLLMLFLGHYLRHKG 360

QY 361 TYLTBEAKGSDDAPDADTALINAEQSGGDDKKEYFI 398
Db 361 TYLTBEAKGSDDAPDADTALINAEQSGGDDKKEYFI 398

RESULT 14
US-09-907-942-84

```

```

; Sequence 84, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-84

```

```

US-09-906-838-84

Query Match          100.0%; Score 2086; DB 10; Length 398;
Best Local Similarity 100.0%; Pred No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAAILLLLLLFFACCAWAPGGANLSQDSSQPWTSDETVAAGTVVLKQVXKDHEDSSL 60
Db 1 MGAPAAAILLLLLLFFACCAWAPGGANLSQDSSQPWTSDETVAAGTVVLKQVXKDHEDSSL 60

QY 61 QWSNPAOQTLTFGEKRALRNRQLVTSSTPHELSISISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAOQTLTFGEKRALRNRQLVTSSTPHELSISISNVALADEGEYTCISFTMPVRTA 120

QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLUNCSSGSKPAARLTWRKQDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLUNCSSGSKPAARLTWRKQDQELHGEPTRIQ 180

QY 181 EDNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSQSRIEVLVYPTAMIRPD 240
Db 181 EDNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSQSRIEVLVYPTAMIRPD 240

QY 241 PPHREGOKLLHCEGRGNPVPQOYLWEKSGVPPKMTQESALIPFPLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCEGRGNPVPQOYLWEKSGVPPKMTQESALIPFPLNKSDSGTYGCT 300

QY 301 ATSNMGSYKAYTTLNVNDSPVPSSSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
Db 301 ATSNMGSYKAYTTLNVNDSPVPSSSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360

QY 361 TYLTHRAKSGDDAPDADTATIIINAEGQSGGDDKKEYFI 398
Db 361 TYLTHRAKSGDDAPDADTATIIINAEGQSGGDDKKEYFI 398

RESULT 13
US-09-907-613-84
; Sequence 84, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

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Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISINVALADEGYTCSIFTMPVRTA 120
Db 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISINVALADEGYTCSIFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSORSORLEVLYTPTAMIRPD 240
Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSORSORLEVLYTPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRGNPVPQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCEGRGNPVPQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYITLVNDPSPVPSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSYKAYITLVNDPSPVPSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
QY 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398

RESULT 11
US-09-906-742-84
; Sequence 84, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-906-742-84

Query Match
Best Local Similarity 100.0%; Score 2086; DB 10; Length 398;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISINVALADEGYTCSIFTMPVRTA 120
Db 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISINVALADEGYTCSIFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSORSORLEVLYTPTAMIRPD 240
Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSORSORLEVLYTPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRGNPVPQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCEGRGNPVPQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYITLVNDPSPVPSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSYKAYITLVNDPSPVPSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
QY 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398

RESULT 12
US-09-906-838-84
; Sequence 84, Application US/09906838

```

APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,841
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 84
 LENGTH: 398
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-907-841-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MCAPASLILLLLLFACCPAGANLSQDSQPMWTSDEFTVAGGTWVLKCKQKDHEDSSL	60
Db	1	MCAPASLILLLLLFACCPAGANLSQDSQPMWTSDEFTVAGGTWVLKCKQKDHEDSSL	60
QY	61	QWSNPAQTLVFGKRALDNRIQLVTSIPHELSSISNVALADGEVTCSTFTMPVETA	120
Db	61	QWSNPAQTLVFGKRALDNRIQLVTSIPHELSSISNVALADGEVTCSTFTMPVETA	120
QY	121	KSLVTVLGIPQKPIITGYKSSLRKXTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
Db	121	KSLVTVLGIPQKPIITGYKSSLRKXTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
QY	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSSTQRIEVLVYPTAMIRPD	240
Db	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSSTQRIEVLVYPTAMIRPD	240
QY	241	PPHREGQKLLHCEGRGNVPQVWLWKEGKSVPLKMTQESALIFPPLNKSDSGTGCT	300
Db	241	PPHREGQKLLHCEGRGNVPQVWLWKEGKSVPLKMTQESALIFPPLNKSDSGTGCT	300
QY	301	ATSNMGSKYATYTLNVNDPSPVSSSTTHAIIIGIVAFIVFLLLIMLIFLGHVLIHKG	360
Db	301	ATSNMGSKYATYTLNVNDPSPVSSSTTHAIIIGIVAFIVFLLLIMLIFLGHVLIHKG	360
QY	361	TYLTHEAKGSDADPADTAIINAEQSGGDDKEYFI	398
Db	361	TYLTHEAKGSDADPADTAIINAEQSGGDDKEYFI	398

RESULT 10
 US-09-904-011-84
 ; Sequence 84, Application US/09904011
 ; Publication No. US20030003530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar P.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/904,011
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 84
 LENGTH: 398
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-904-011-84

Query Match 100.0%; Score 2086; DB 10; Length 398;

Qy 361 TYLTHEAKGSDADPADTAINAEGSGGDDKKKEYFI 398
 Db 361 TYLTHEAKGSDADPADTAINAEGSGGDDKKKEYFI 398

RESULT 8
 US-09-907-824-84
 ; Sequence 84, Application US/09907824
 ; Publication No. US20020197671A1
 GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptide
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907,824
 ; PRIOR FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 60/095,672
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-778-187B-10

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDETVVAGGTVVLKCOVKDHESSSL	60
Db	1	MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDETVVAGGTVVLKCOVKDHESSSL	60
Qy	61	QWSNPAQQTLYFGEKRALRDNRILQVSTPHELSSISINVALADEGEYTCSTFTMPVRTA	120
Db	61	QWSNPAQQTLYFGEKRALRDNRILQVSTPHELSSISINVALADEGEYTCSTFTMPVRTA	120
Qy	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
Db	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
Qy	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADSTQRIEVLVYPTAMIRPD	240
Db	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADSTQRIEVLVYPTAMIRPD	240
Qy	241	PPHREGQKLLHCEGRGNVPQOYLWEKESVPLPKMTQESALIFPFLNKSDSGTYGCT	300
Db	241	PPHREGQKLLHCEGRGNVPQOYLWEKESVPLPKMTQESALIFPFLNKSDSGTYGCT	300
Qy	301	ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKG	360
Db	301	ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKG	360
Qy	361	TYLTHEAKGSDPADADATATINARGGSGGDDKKEYFI	398
Db	361	TYLTHEAKGSDPADADATATINARGGSGGDDKKEYFI	398

RESULT 7

US-09-902-853-84
 ; Sequence 84, Application US/09902853
 ; Publication No. US20020192659A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/902,853
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US/09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 84
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-902-853-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDETVVAGGTVVLKCOVKDHESSSL	60
Db	1	MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDETVVAGGTVVLKCOVKDHESSSL	60
Qy	61	QWSNPAQQTLYFGEKRALRDNRILQVSTPHELSSISINVALADEGEYTCSTFTMPVRTA	120
Db	61	QWSNPAQQTLYFGEKRALRDNRILQVSTPHELSSISINVALADEGEYTCSTFTMPVRTA	120
Qy	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
Db	121	KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ	180
Qy	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADSTQRIEVLVYPTAMIRPD	240
Db	181	EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADSTQRIEVLVYPTAMIRPD	240
Qy	241	PPHREGQKLLHCEGRGNVPQOYLWEKESVPLPKMTQESALIFPFLNKSDSGTYGCT	300
Db	241	PPHREGQKLLHCEGRGNVPQOYLWEKESVPLPKMTQESALIFPFLNKSDSGTYGCT	300
Qy	301	ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKG	360
Db	301	ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKG	360

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 84
;; LENGTH: 398
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-905-291A-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVWAGGTVVLKQVCKDHDSSSL 60
DB 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVWAGGTVVLKQVCKDHDSSSL 60

QY 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISNNVALADEGEYTCSTFTMPVRTA 120
DB 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISNNVALADEGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQ 180
DB 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQ 180

QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIVELYTPTAMIRPD 240
DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIVELYTPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNVPVQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGQKLLHCEGRGNVPVQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360

RESULT 6

US-09-778-187b-10
; Sequence 10, Application US/09778187b
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187b
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05

QY 361 TYLTAEKSGDDADPADTATINAEQGSGGDDKKEYFI 398
DB 361 TYLTAEKSGDDADPADTATINAEQGSGGDDKKEYFI 398

RESULT 5
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. US20020164866A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVWAGGTVVLKQVCKDHDSSSL 60
DB 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVWAGGTVVLKQVCKDHDSSSL 60

QY 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISNNVALADEGEYTCSTFTMPVRTA 120
DB 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISNNVALADEGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQ 180
DB 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQ 180

QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIVELYTPTAMIRPD 240
DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIVELYTPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNVPVQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGQKLLHCEGRGNVPVQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360

QY 361 TYLTAEKSGDDADPADTATINAEQGSGGDDKKEYFI 398
DB 361 TYLTAEKSGDDADPADTATINAEQGSGGDDKKEYFI 398

QY 361 TYLTAEKSGSDADPADTATINAEQSGGDDKKEYFI 398
 Db 361 TYLTAEKSGSDADPADTATINAEQSGGDDKKEYFI 398

RESULT 3

US-09-909-088B-84
 ; Sequence 84, Application US/09909088B
 ; Patent No. US20020146709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Christopher J.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/909, 088B
 ; CURRENT FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 84
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-909-088B-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPASLLLLLLFACCCWAPGAGANLSQDSSQWTSDETVVAGTTLKQVQKHEDSSL 60
 Db 1 MGAPASLLLLLLFACCCWAPGAGANLSQDSSQWTSDETVVAGTTLKQVQKHEDSSL 60
 QY 61 QWSNPAQQTLYFGKEKALNRRIQLVTSFPHLSISISNVALADEGEYTCSTFMPVTA 120
 Db 61 QWSNPAQQTLYFGKEKALNRRIQLVTSFPHLSISISNVALADEGEYTCSTFMPVTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLPREKDTATLNCSSGSKPAARLTWRKQDELHGEPTRIQ 180
 Db 121 KSLVTVLGIPQKPIITGYKSSLPREKDTATLNCSSGSKPAARLTWRKQDELHGEPTRIQ 180
 QY 181 EDNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTQRIEVLVYPTAMIRPD 240
 Db 181 EDNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTQRIEVLVYPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGNGNVPQOYLWEKEGSGVPLKMTQESALIFPELNKSDSGTYGCT 300
 Db 241 PPHREGQKLLHCEGNGNVPQOYLWEKEGSGVPLKMTQESALIFPELNKSDSGTYGCT 300
 QY 301 ATSNMGSYKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLMLFLGHLIRHKG 360
 Db 301 ATSNMGSYKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLMLFLGHLIRHKG 360
 QY 361 TYLTAEKSGSDADPADTATINAEQSGGDDKKEYFI 398
 Db 361 TYLTAEKSGSDADPADTATINAEQSGGDDKKEYFI 398

RESULT 4

US-09-905-291A-84
 ; Sequence 84, Application US/09905291A
 ; Patent No. US20020160374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

; INFORMATION FOR SEQ ID NO: 102:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 398 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-745-763-102

Query Match          100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSDQWTSDETVVAGTGVVLKQVQKHEDSSSL 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSDQWTSDETVVAGTGVVLKQVQKHEDSSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120
DB 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPOKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
DB 121 KSLVTVLGIPOKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSQSRIEVLVYPTAMIRPD 240
DB 181 EDPNGKTFVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSQSRIEVLVYPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRNPNVQYQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGOKLLHCEGRNPNVQYQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
QY 361 TYLTHEAKSGDDAPDADTAIINAEGQSGGDDKKKEYFI 398
DB 361 TYLTHEAKSGDDAPDADTAIINAEGQSGGDDKKKEYFI 398

RESULT 2
US-09-909-320-84
; Sequence 84, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
;   APPLICANT: Genentech, Inc.
;   APPLICANT: Ashkenazi, Avi
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Gerber, Hanspeter
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, A.
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth, J.
;   APPLICANT: Kijavich, Ivar J.
;   APPLICANT: Mather, Jennie P.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William, I.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: 10466-14
;   CURRENT APPLICATION NUMBER: US/09/909,320
;   CURRENT FILING DATE: 2002-01-04
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: 2000-02-22
;   PRIOR APPLICATION NUMBER: US 60/143,048
;   PRIOR FILING DATE: 1999-07-07
;   PRIOR APPLICATION NUMBER: US 60/145,698
;   PRIOR FILING DATE: 1999-07-26
;   PRIOR APPLICATION NUMBER: US 60/146,222
;   PRIOR FILING DATE: 1999-07-28
;   PRIOR APPLICATION NUMBER: PCT/US99/20594
;   PRIOR FILING DATE: 1999-09-08
;   PRIOR APPLICATION NUMBER: PCT/US99/20944
;   PRIOR FILING DATE: 1999-09-13
;   PRIOR APPLICATION NUMBER: PCT/US99/21090
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: PCT/US99/21547
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: PCT/US99/23089
;   PRIOR FILING DATE: 1999-10-05
;   PRIOR APPLICATION NUMBER: PCT/US99/28214
;   PRIOR FILING DATE: 1999-11-29
;   PRIOR APPLICATION NUMBER: PCT/US99/28313
;   PRIOR FILING DATE: 1999-11-30
;   PRIOR APPLICATION NUMBER: PCT/US99/28564
;   PRIOR FILING DATE: 1999-12-02
;   PRIOR APPLICATION NUMBER: PCT/US99/28565
;   PRIOR FILING DATE: 1999-12-02
;   PRIOR APPLICATION NUMBER: PCT/US99/30095
;   PRIOR FILING DATE: 1999-12-16
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;   PRIOR FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US99/30999
;   PRIOR FILING DATE: 1999-12-20
;   PRIOR APPLICATION NUMBER: PCT/US00/00219
;   PRIOR FILING DATE: 2000-01-05
;   NUMBER OF SEQ ID NOS: 423
;   SEQ ID NO 84
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   US-09-909-320-84

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DB 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-778-187B-10

Perfect score: 2086

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2086	100.0	398	9	US-09-905-291A-84
5	2086	100.0	398	9	US-09-778-510-6
6	2086	100.0	398	9	US-09-778-187B-10
7	2086	100.0	398	9	US-09-902-853-84
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ALIGNMENTS

RESULT 1

US-09-745-763-102
; Sequence 102, Application US/09745763
; Patent No. US20020065394A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
McCoy, John M.
Lavallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 219

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/745.763

FILING DATE: 18-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.

REGISTRATION NUMBER: 41,323

TELECOMMUNICATION INFORMATION:

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TELEFAX: (617) 876-5851

Thu May 27 10:42:49 2004

us-09-778-187b-10.rag

Query Match 100.0%; Score 2086; DB 6; Length 398;
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XX 06-MAY-2002; 2002US-00140474.
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US016824.
PR 14-SEP-1998; 98WO-US013093.
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PR 14-SEP-1998; 98WO-US013177.
PR 16-SEP-1998; 98WO-US013330.
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PR 29-OCT-1998; 98WO-US022991.
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PR 18-MAY-2001; 2001US-00860216.
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PR 25-MAY-2001; 2001WO-US017092.
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PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski FJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

WPI: 2003-341980/32.

N-PSDB; ACD24026.

PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.

XX Claim 12; Fig 348; 560pp; English.

CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

XX Sequence 398 AA;

PR 28-OCT-1997; 97US-0063544P.
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 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
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 PR 07-NOV-1997; 97US-0064809P.
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 PR 17-NOV-1997; 97US-0065846P.
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 PR 21-NOV-1997; 97US-0066120P.
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 PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mathew JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI: 2003-328338/31.
 DR N-PSDB; ACAS8964.

XX Isolated nucleic acid useful for e.g., treating pathological disorders
 PT encodes a secreted or transmembrane protein.

XX Claim 12; Fig 32; 473pp; English.

XX The invention relates to human PRO polypeptides (secreted or

CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC PRO polypeptides and polynucleotides can be used in treating pathological
 CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
 CC disorders and in therapeutic treatment of disorders involving protein
 CC secretion by the pancreas, including diabetes. They can also be used in
 CC treating disorders associated with the preservation and maintenance of
 CC gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, and skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g., psoriasis, epithelial cancers such as lung
 CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
 CC The sequences can be used as molecular markers for protein
 CC electrophoresis purposes and can be utilised in protein-protein binding
 CC assays, biochemical screening assays, immunoassays and cell-based assays.
 CC This sequence represents a human PRO polypeptide of the invention

XX Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 6; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - MGAPAAALLLLLLFACCAWAPGGANLSQDDSQPWTSDTTVAGTVVLKQVKHEDSSL 60
 DB - MGAPAAALLLLLLFACCAWAPGGANLSQDDSQPWTSDTTVAGTVVLKQVKHEDSSL 60
 QY 61 QWSNPAQQTLYFGKRALRDNRIOIVTSTPHELSTISINVALADEGYTCSTFTMPVETA 120
 DB 61 QWSNPAQQTLYFGKRALRDNRIOIVTSTPHELSTISINVALADEGYTCSTFTMPVETA 120
 QY 121 KSLVTVLGIPQKIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPETRIQ 180
 DB 121 KSLVTVLGIPQKIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPETRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTQRIEVLVPTTAMIRPD 240
 DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTQRIEVLVPTTAMIRPD 240
 QY 241 PPHREGOKLLHCEGRGNPVPQQYLWEKESVPLKMTQESALIFPFLNKSDSTYGTCT 300
 DB 241 PPHREGOKLLHCEGRGNPVPQQYLWEKESVPLKMTQESALIFPFLNKSDSTYGTCT 300
 QY 301 ATSNMGSKAYTYLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
 DB 301 ATSNMGSKAYTYLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
 QY 361 TYLTAEAKGSDADPADTAIINAEKGSGGDDKKEYFI 398
 DB 361 TYLTAEAKGSDADPADTAIINAEKGSGGDDKKEYFI 398

RESULT 15

ABO17789

ID ABO17789 standard; protein; 398 AA.

XX ABO17789;

AC ABO17789;

DT 26-AUG-2003 (first entry)

XX

XX Novel human secreted and transmembrane protein PRO258.

DE Human; secreted and transmembrane protein; PRO; antiinflammatory;
 XX antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.

OS Homo sapiens.

XX

PI XX US2002065394-A1.
 PD XX 30-MAY-2002.
 PE PF 22-DEC-2000; 2000US-00745763.
 XX XX 18-MAR-1998; 98US-00040963.
 XX XX (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREA/) TREACY M.
 PA (SPAU/) SPAULDING V.
 XX XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Spaulding V;
 XX XX WPI; 2002-582343/62.
 DR N-PSDB; ABQ92039.
 XX XX
 PT Novel secreted or transmembrane protein and polynucleotide encoding the
 PT protein, useful for diagnosis and treatment of neurological disorders,
 PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
 PS
 PS Claim 130; Page 154-155; 284pp; English.
 XX
 CC The invention relates to human secreted or transmembrane protein (I),
 CC their fragments and is encoded by specific complementary deoxyribonucleic
 CC acid (cDNA) inserts (II), where the protein is substantially free from
 CC other mammalian proteins. (I) are useful for preventing, treating or
 CC ameliorating a medical condition, especially immunological treatment or
 CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity and activin or inhibin-related
 CC activities. (I) can be used to manipulate stem cells in culture to give
 CC rise to neuroepithelial cells that can be used to augment or replace
 CC cells damaged by illness, autoimmune disease, accidental damage or
 CC genetic disorders. (I) induces the proliferation of neural cells and
 CC regeneration of nerve and brain tissue and is useful for the treatment of
 CC central and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopaenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
 CC periodontal disease. (I) is also useful for gut protection or
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
 CC in various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
 CC such as asthma or other respiratory problems. (II) is useful to express
 CC recombinant protein, as markers for tissues in which the corresponding
 CC protein is preferentially expressed and in gene therapy. The present
 CC sequence is that of a polypeptide of the invention
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 5; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNPRAALILLLFACCAWPGANLSQDSQFWSDETVAAGTVLKCQVKHEDSSL 60
 DB 1 MGNPRAALILLLFACCAWPGANLSQDSQFWSDETVAAGTVLKCQVKHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSTPHLSISISNVALADEGEYTCSTFTMPVTA 120

DB 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSTPHLSISISNVALADEGEYTCSTFTMPVTA 120
 QY 121 KSLVTVLGIPOKEPIITGYKSLREKDTATINCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPOKEPIITGYKSLREKDTATINCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQISQIEVLVYTPMTAMIRPD 240
 DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQISQIEVLVYTPMTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGVPPLKMTQESALIPFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGVPPLKMTQESALIPFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDSPVSSSTVHAIIIGGIVAFIVFLLLMFLFGLHYLRHKG 360
 DB 301 ATSNMGSKAYTYTLNVNDSPVSSSTVHAIIIGGIVAFIVFLLLMFLFGLHYLRHKG 360
 QY 361 TYLTHEAKGSDDAPDADTAIINAEGGSGDDKKEYFI 398
 DB 361 TYLTHEAKGSDDAPDADTAIINAEGGSGDDKKEYFI 398
 RESULT 14
 ABU71604
 ID ABU71604 standard; protein; 398 AA.
 XX AC ABU71604;
 XX DT 16-JUN-2003 (first entry)
 XX DE Human PRO polypeptide #15.
 XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW pathological disorder; cardiac insufficiency disorder; protein secretion;
 KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
 KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
 KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
 KW cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal;
 KW antiulcer; dermatological; vulnary.
 XX OS Homo sapiens.
 XX PN US2002146709-A1.
 XX PD 10-OCT-2002.
 XX PF 18-JUL-2001; 2001US-00909088.
 XX PR 17-SEP-1997; 97US-00591113P.
 PR 17-SEP-1997; 97US-00591115P.
 PR 17-SEP-1997; 97US-00591117P.
 PR 17-SEP-1997; 97US-00591119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.

Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
cardiant; cytostatic; antiangiogenic; hypotensive; vulnery;

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 44; 567pp; English.

The present invention provides the protein and coding sequences of human
PRO proteins. These are useful for treating or diagnosing a
cardiovascular, endothelial or angiogenic disorder, including cardiac
hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The present sequence is a PRO protein of the invention

Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.5e-149;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGAPAAASLLLLLLFACWAPCGANLSQDDSPQWTSDETVVAGGVVLCQVKDHEDSSL	60
DB	1	MGAPAAASLLLLLLFACWAPCGANLSQDDSPQWTSDETVVAGGVVLCQVKDHEDSSL	60
QY	61	QWSNPAQOTLYFGEKRALDNRIOQVSTPHLSISINVALADEGYTCSTFTMPVRTA	120
DB	61	QWSNPAQOTLYFGEKRALDNRIOQVSTPHLSISINVALADEGYTCSTFTMPVRTA	120
QY	121	KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ	180
DB	121	KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ	180
QY	181	EDPNGKTFVSSVTFQVTRDDGASIVCSNVHESLKADRTSQRIVLYPTAMIRPD	240
DB	181	EDPNGKTFVSSVTFQVTRDDGASIVCSNVHESLKADRTSQRIVLYPTAMIRPD	240
QY	241	PPHPREGQKLLHCEGRGNVPVQQLWKEGSPVPLKMTQESALIFPFLNKSDSTGYCT	300
DB	241	PPHPREGQKLLHCEGRGNVPVQQLWKEGSPVPLKMTQESALIFPFLNKSDSTGYCT	300
QY	301	ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG	360
DB	301	ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG	360
QY	361	TYLTHEAKGSDDAPDADTAITNAEGGQSGDDKKEYFI	398
DB	361	TYLTHEAKGSDDAPDADTAITNAEGGQSGDDKKEYFI	398

RESULT 13

ABP61823

ID ABP61823 standard; protein; 398 AA.

AC ABP61823;

DT 04-OCT-2002 (first entry)

DE Human polypeptide SEQ ID NO 177.

Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;
antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;
immunostimulant; antiparasitic; secreted protein; transmembrane protein;
cytokine; cell proliferation; cell differentiation; autoimmune disease;
stem cell; growth factor; nervous system disease; neuropathy;
Alzheimer's disease; Parkinson's disease; Huntington's disease;
osteoporosis; severe combined immunodeficiency; SCID; infection;
multiple sclerosis; rheumatoid arthritis; gene therapy.

Homo sapiens.

OS

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX

PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222595P.
PR 17-AUG-2000; 2000US-0224365P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242322P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 20-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

(GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATP/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95582.
XX

Db 301 ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLIMLIFLGHYLIRHKG 360
 QY 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398
 Db 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398

RESULT 11
 ID ABB84838 standard; protein; 398 AA.
 AC ABB84838;
 XX
 DT 16-MAY-2002 (first entry)
 DE Human PRO258 protein sequence SEQ ID NO:44.

Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;
 vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 age-related macular degeneration; arterial restenosis; angina;
 rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 28-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 01-MAR-2001; 2001WO-US006520.

XX 09-MAR-2001; 2001WO-US006666.

XX 14-MAR-2001; 2001US-00802706.

XX 22-MAR-2001; 2001US-00808689.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;
 XX WPI; 2002-090516/12.
 XX N-PSDB; ABL88093.
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 44; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 XX Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 5; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDTAVAGTIVLKQVKHEDSSL 60
 Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDTAVAGTIVLKQVKHEDSSL 60
 QY 61 QWSNPAQQTLYFGEKRALDNRILQVTSHPHELSISINVALADEGEYTCSTFTMPVRTA 120
 Db 61 QWSNPAQQTLYFGEKRALDNRILQVTSHPHELSISINVALADEGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 Db 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTSORIEVLTPYTPMIRPD 240
 Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTSORIEVLTPYTPMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNPVPQVLMKEGKSVPLKMTQESALIFPFLNKSDSGTYGCT 300
 Db 241 PPHREGQKLLHCEGRGNPVPQVLMKEGKSVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLIMLIFLGHYLIRHKG 360
 Db 301 ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLIMLIFLGHYLIRHKG 360
 QY 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398
 Db 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398

RESULT 12

ABB95444

ID ABB95444 standard; protein; 398 AA.

XX ABB95444;

AC ABB95444;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO258 SEQ ID NO: 44.

XX

QY 1 MGAPAAALLLLLLLFFACWAPGANLSDSQPMTSDTAVAGGTWLVKCKQVQKHEDSSL 60
 DB 1 MGAPAAALLLLLLLFFACWAPGANLSDSQPMTSDTAVAGGTWLVKCKQVQKHEDSSL 60
 QY 61 QWSNPAQQTLYFGEKRALDRNRIOQLVSTPHLSISISNVALADEGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQQTLYFGEKRALDRNRIOQLVSTPHLSISISNVALADEGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADRTSQRILEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADRTSQRILEVLYTPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDPSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIHRKG 360
 DB 301 ATSNMGSKAYTYTLNVNDPSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIHRKG 360
 QY 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398
 DB 361 TYLTAEKSGDDAPDADTAIINAEQSGGDDKKEYFI 398
 RESULT 10
 ID AAB53083
 XX AC AAB53083;
 XX DT 28-FEB-2001 (first entry)
 XX DE Human angiogenesis-associated protein PRO258, SEQ ID NO:101.
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 OS Homo sapiens.
 XX FN WO200053753-A2.
 XX PD 14-SEP-2000.
 XX PF 05-JAN-2000; 2000WO-US000219.
 XX PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 05-OCT-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US023089.
 PR 02-DEC-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.

(GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WL;
 WPI: 2001-090793/10.
 DR N-PSDB; AAC97445.
 XX
 New isolated nucleic acid for producing a PRO polypeptide, analyzing
 genetic disorders and treating cardiovascular, endothelial or angiogenic
 disorders, such as atherosclerosis, wounds or cancer.
 PS Claim 69; Fig 40; 23pp; English.
 XX
 The invention relates to novel human angiogenesis-associated proteins
 designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 PRO proteins. The invention also relates to vectors and host cells
 comprising a PRO nucleic acid, the recombinant production of a PRO
 protein, PRO antibodies specific for a PRO protein, fusion proteins
 comprising a PRO protein, agonists or antagonists of a PRO protein, and
 compounds which inhibit the expression of a PRO gene. The invention
 additionally encompasses methods of identifying modulators of PRO
 expression or activity; diagnosing a cardiovascular, endothelial or
 angiogenic disorder, or a susceptibility to such a disorder by detecting
 mutations in a PRO gene, or the expression level of a PRO gene within a
 particular tissue; treating a cardiovascular, endothelial or angiogenic
 disorder via the administration of a PRO protein, PRO nucleic acid, or
 PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 administration of a PRO protein, or an agonist or antagonist thereof. PRO
 nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 agonists and PRO antagonists may be used as therapeutic agents to treat
 cardiovascular, endothelial or angiogenic disorders, such as
 atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 disease, or stroke. PRO nucleic acids are additionally useful in the
 recombinant production of PRO proteins, as hybridisation probes to screen
 libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 genes encoding PRO proteins, to analyse genetic disorders, and in gene
 therapy. PRO nucleic acids can also be used to produce transgenic animals
 useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention
 XX
 SQ Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLLFFACWAPGANLSDSQPMTSDTAVAGGTWLVKCKQVQKHEDSSL 60
 DB 1 MGAPAAALLLLLLLFFACWAPGANLSDSQPMTSDTAVAGGTWLVKCKQVQKHEDSSL 60
 QY 61 QWSNPAQQTLYFGEKRALDRNRIOQLVSTPHLSISISNVALADEGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQQTLYFGEKRALDRNRIOQLVSTPHLSISISNVALADEGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADRTSQRILEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSKLGADRTSQRILEVLYTPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDPSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIHRKG 360

CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLFFACCAWAGANLQDDSQPWTSDTAVAGTVVLCQVKQKHEDSSL 60
 Db 1 MGAPAAASLLLLLFFACCAWAGANLQDDSQPWTSDTAVAGTVVLCQVKQKHEDSSL 60
 QY 61 QWSNPAQOTLYGEXKRALDNRIOQVTSPPHELSSISINVALADGEGYTCSTFTMPVRTA 120
 Db 61 QWSNPAQOTLYGEXKRALDNRIOQVTSPPHELSSISINVALADGEGYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPOKPIITGYKSLUREKDTATLNCOSGSKPAARLTWRKGDQELHGEPTRIQ 180
 Db 121 KSLVTVLGIPOKPIITGYKSLUREKDTATLNCOSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPD 240
 Db 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPD 240
 QY 241 PPHREGOKLLHCHGRGNPVPQOYLWEKGSVPLKMTQESALFPFLNKSDSGTYGCT 300
 Db 241 PPHREGOKLLHCHGRGNPVPQOYLWEKGSVPLKMTQESALFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYITLVNDPSPVSSSTVHAIGGIVAFIVFLLIMLIFLGHYLIRHKG 360
 Db 301 ATSNMGSKAYITLVNDPSPVSSSTVHAIGGIVAFIVFLLIMLIFLGHYLIRHKG 360
 QY 361 TYLTAEKSGDDAPADTAIINAEQSGSGGDDKKEVFI 398
 Db 361 TYLTAEKSGDDAPADTAIINAEQSGSGGDDKKEVFI 398
 RESULT 9
 AAU12345
 ID AAU12345 standard; protein; 398 AA.
 XX AC AAU12345;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO258 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200140466-A2.
 XX PD 07-JUN-2001.
 XX PF 01-DEC-2000; 2000WO-US032678.
 XX PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21417.
 XX Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX Claim 12; Fig 348; 813pp; English.
 PS AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 diabetes; stroke; gene therapy; transgenic; PRO; human.

OS Homo sapiens.
 XX WO200015796-A2.
 PN 23-MAR-2000.
 PD 15-SEP-1999; 99WO-US021090.
 XX 16-SEP-1998; 98WO-US019330.
 XX (GETH) GENENTECH INC.
 PA Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX WPI: 2000-271434/23.
 DR N-PSDB; ADC78403.
 XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX Claim 12; SEQ ID NO 84; 355pp; English.
 XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, rheumatoid arthritis, multiple
 CC cartilage formation, angiogenesis, asthma, thrombosis, bone and/or
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO protein of the invention.

XX Sequence 398 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 2086; DB 3; Length 398;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAALLLLLLLFFACWAPGAGNLQDDSPWTSDETIVAGTVLKCQVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLFFACWAPGAGNLQDDSPWTSDETIVAGTVLKCQVKHEDSSL 60
 QY 61 QWSNPAQOTLFGKRRALDNRIQVTSPEHLSISINVALADGEXTCSFTFMPVETA 120
 DB 61 QWSNPAQOTLFGKRRALDNRIQVTSPEHLSISINVALADGEXTCSFTFMPVETA 120
 QY 121 KSLVTVLGIPQPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180
 DB 121 KSLVTVLGIPQPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTTREDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
 DB 181 EDPNGKTFVSSSVTFQVTTREDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
 QY 241 PPHREGKLLHLCGRGNVPQVYLWKEGSPVPLKMTQSSALFPFLNKSDSGTYGCT 300
 DB 241 PPHREGKLLHLCGRGNVPQVYLWKEGSPVPLKMTQSSALFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYLNVNDPSPVPSSSTYHALIGIVAFIVFLLLIMLIFLGHYLIHRKG 360
 DB 301 ATSNMGSKAYTYLNVNDPSPVPSSSTYHALIGIVAFIVFLLLIMLIFLGHYLIHRKG 360

QY 361 TYLTHEAKGSDPADPADTALINAEQGSGGDDKKEYFI 398
 DB 361 TYLTHEAKGSDPADPADTALINAEQGSGGDDKKEYFI 398

RESULT 8
 AAB80226
 ID AAB80226 standard; protein; 398 AA.
 XX AC AAB80226;
 XX DT 24-APR-2001 (first entry)
 XX Human PRO258 protein.
 DE Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 XX KW antiparkinsonian nootropic; neuroprotective; vulnary; cardiac;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX OS Homo sapiens.
 XX PN WO200104311-A1.
 XX PD 18-JAN-2001.
 XX PF 22-FEB-2000; 2000WO-US004414.
 XX 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather CP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI: 2001-081051/09.
 DR N-PSDB; AAF72387.
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX Claim 1; Fig 32; 393pp; English.
 CC The present sequence is one of sixty one novel secreted and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory

CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic
 CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes
 CC which catalyze a colorimetric or fluorometric reaction, may be attached
 CC to a B7L-1 polypeptide, e.g. nitrogen mustards are attached to the B7L-1
 CC and used to treat various forms of cancer
 XX

SQ Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 3; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLLPACWAPGGANLSDQDSQPWTSDETVVAGGVVLKQVKDHEDSSL 60
 DB 1 MGAPAAASLLLLLLLPACWAPGGANLSDQDSQPWTSDETVVAGGVVLKQVKDHEDSSL 60

QY 61 QWSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180

QY 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHSLKGADRSQRIEVLVYPTAMIRPD 240
 DB 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHSLKGADRSQRIEVLVYPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHVLIIRHG 360
 DB 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHVLIIRHG 360

QY 361 TYLTAEAGSDADPADTAIINAEQGSGGDDKKEYFI 398
 DB 361 TYLTAEAGSDADPADTAIINAEQGSGGDDKKEYFI 398

RESULT 6

AAV45095
 ID AAV45095 standard; protein; 398 AA.

AC AAV45095;

XX 31-MAY-2000 (first entry)

DE Human LDCAM binding protein, B7L-1 short form.

XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-L1;
 KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
 KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.

OS Homo sapiens.

XX WO200008158-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99WO-US017905.

XX 07-AUG-1998; 98US-0095672P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC;

XX WPI; 2000-205712/18.

DR N-PSDB; AAZ50687.

XX Novel molecules designated LDCAM are capable of altering or modulating T
 PT cell function.

PS Disclosure; Page 53-54; 44pp; English.

XX The present amino acid sequence is the human LDCAM (lymphoid derived
 CC dendritic cell adhesion molecule) binding protein, B7L-1 short form. B7L
 CC -1 has sequence similarity to adhesion molecule, B7-1. B7L-1 and LDCAM
 CC display homology within their intracellular domain, found on many of the
 CC same cell types and their cell-bound forms deliver signals when
 CC engaged and are termed as co-receptors or counter structures. LDCAM
 CC polypeptides interacts with T cell surface molecules to alter signalling
 CC and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM
 CC binding protein and increases natural killer (NK) cell populations. It
 CC may be used to measure the biological activity and as quality control
 CC reagents of LDCAM binding proteins. LDCAM may be used for treating
 CC disorders associated with malfunctioning of immune system, inflammation,
 CC autoimmune disorders, viral infected cells, infectious diseases and for
 CC killing tumour cells. They are also useful for prevention or reducing the
 CC effect of organ and bone marrow transplant rejection and for modulating T
 CC cell immune responses. LDCAM polypeptides may also be used as carriers
 CC for delivering agents attached to T cells or cells bearing B7L-1

XX Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 3; Length 398;

Best Local Similarity 100.0%; Pred. No. 4.5e-149;

Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLLPACWAPGGANLSDQDSQPWTSDETVVAGGVVLKQVKDHEDSSL 60

DB 1 MGAPAAASLLLLLLLPACWAPGGANLSDQDSQPWTSDETVVAGGVVLKQVKDHEDSSL 60

QY 61 QWSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120

DB 61 QWSNPAQOTLYFGEKRALDRNRQLVSTPHELSSISINVALADEGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180

DB 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180

QY 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHSLKGADRSQRIEVLVYPTAMIRPD 240

DB 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHSLKGADRSQRIEVLVYPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300

DB 241 PPHREGQKLLHCEGRGNVPVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHVLIIRHG 360

DB 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHVLIIRHG 360

QY 361 TYLTAEAGSDADPADTAIINAEQGSGGDDKKEYFI 398

DB 361 TYLTAEAGSDADPADTAIINAEQGSGGDDKKEYFI 398

RESULT 7

ADC78404

ID ADC78404 standard; protein; 398 AA.

AC ADC78404;

XX 01-JAN-2004 (first entry)

XX Human PRO258 protein.

XX antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthmatic; antidiabetic; antirheumatic;
 KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;

KW Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
 KW neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
 KW dementia; epilepsy; schizophrenia; peripheral nerve injury;
 KW diabetic neuropathy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Signal_peptide
 FT Protein 25..398
 FT /label= ACAM
 XX WO200032633-A1.
 PN 08-JUN-2000.
 PD 02-DEC-1999; 99WO-US028878.
 XX 02-DEC-1998; 98US-00203462.
 PR (ICOS-) ICOS CORP.
 PA Hoekstra DM, Loughney K, Stauton DE, Vazeux R;
 XX WPI; 2000-422952/36.
 DR N-PSDB; AAY94403.
 XX Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
 PT for diagnosing, preventing and treating diseases associated with ACAM
 PT expression and activity, e.g. epilepsy and schizophrenia.
 XX Claim 5; Page 149-150; 187pp; English.
 XX The present sequence is a novel adhesion molecule, designated ACAM. The
 CC full-length nucleotide sequence was identified in clone ACAM4 of a human
 CC foetal brain library. The polypeptide is 100% homologous to the
 CC polypeptide encoded by clone ACAM6 (AAA30423) from the same library
 CC except that it contains a 34 amino acid deletion. It is believed to
 CC correspond to an alternative form of ACAM. The nucleotide sequence and
 CC the protein it encodes may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate ACAM expression and
 CC activity such as dementia, epilepsy, schizophrenia, peripheral nerve
 CC injuries and diabetic neuropathies. They may be used to rectify mutations
 CC or deletions in a patient's genome that affect the activity of ACAM or to
 CC supplement insufficient ACAM production in a patient. The nucleotide
 CC sequence may be integrated into an expression vector and inserted into a
 CC host cell for protein expression in vitro or in vivo. Conversely,
 CC antisense nucleic acid molecules may be administered to down-regulate
 CC ACAM expression. The nucleotide sequence may also be used as a DNA probe
 CC in diagnostic assays (e.g. PCR) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and hence determine which
 CC patients may be in need of restorative therapy. ACAM polypeptides may be
 CC used as antigens in the production of antibodies against ACAM and in
 CC assays to identify modulators (agonists and antagonists) of ACAM
 CC expression and activity
 XX Sequence 398 AA;
 SQ Query Match 100.0%; Score 2086; DB 3; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLLACCCWAGANLSDQSPWTSDETVVAGGTVLKCQVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLACCCWAGANLSDQSPWTSDETVVAGGTVLKCQVKHEDSSL 60
 QY 61 QWSNPAQQLTYFGEKRALRDNRILQVTSPPHELSISISNVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQQLTYFGEKRALRDNRILQVTSPPHELSISISNVALADGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPOKPIITGVKSSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180

DB 121 KSLVTVLGIPOKPIITGVKSSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADSTSORIEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHPREGOKLLHCEGRGNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHPREGOKLLHCEGRGNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSYKAYITLNVNDPSPVSSSTYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
 DB 301 ATSNMGSYKAYITLNVNDPSPVSSSTYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
 QY 361 TYLTHEAKGSDADPADTATLINAEGSGGGDDKKEYFI 398
 DB 361 TYLTHEAKGSDADPADTATLINAEGSGGGDDKKEYFI 398
 RESULT 5
 AAY69288
 ID AAY69288 standard; protein; 398 AA.
 XX AC AAY69288;
 XX DT 19-JUN-2000 (first entry)
 XX DE Amino acid sequence of extracellular form of human B7-1 (CD80).
 XX KW Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
 KW CD28; CTLA4; T cell surface receptor; cytokine production;
 KW cell proliferation; T cell; infection; autoimmune disease; inflammation;
 KW quality assurance; cancer.
 XX OS Homo sapiens.
 XX PN WO200008057-A2.
 XX PD 17-FEB-2000.
 XX PF 05-AUG-1999; 99WO-US017906.
 PR 07-AUG-1999; 98US-0095663P.
 PA (IMMV) IMMUNEX CORP.
 PI Baum PR;
 XX WPI; 2000-205674/18.
 DR N-PSDB; AAZ61418.
 XX Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 PT costimulatory molecules for therapeutics against infections, autoimmune
 PT diseases and inflammation.
 XX Claim 8; Page 47-48; 57pp; English.
 XX The present sequence represents the short extracellular form of human B7-
 CC 1 (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine
 CC production, cell proliferation, and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the disordered mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting

XX Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophla areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX Homo sapiens.
 OS WO99143328-A2.
 PN 25-MAR-1999.
 PD 16-SEP-1998; 98WO-US019330.
 PF 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 21-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063354P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063335P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 XX (GETH) GENENTECH INC.
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 FI WPI; 1999-229533/19.
 XX

DR N-PSDB; AAX52229.
 XX New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration.
 XX Claim 12; Fig 32; 320pp; English.
 PS AAY13344-403 represent secreted and transmembrane human proteins. The
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO333 may
 CC be used in the treatment of Usher Syndrome or Atrophla areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX Sequence 398 AA;
 SQ

Query Match 100.0%; Score 2086; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MCAPAAASLLLLLLFACCAWAGGANLSQDDSQPWTSDTAVAGTVVLKQVKHEDSSL 60
 1 MCAPAAASLLLLLLFACCAWAGGANLSQDDSQPWTSDTAVAGTVVLKQVKHEDSSL 60
 61 QWSNPAQOTLYFGKRALRDNRIOLVSTPHELSTISNVALADEGEVTCSTFTMPVETA 120
 61 QWSNPAQOTLYFGKRALRDNRIOLVSTPHELSTISNVALADEGEVTCSTFTMPVETA 120
 121 KSLVTVLGIPQKIITGYKSSLEKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 121 KSLVTVLGIPQKIITGYKSSLEKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSNVHESLKGADSTSORIEVLYTPTAMIRPD 240
 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSNVHESLKGADSTSORIEVLYTPTAMIRPD 240
 241 PPHREGOKLLHCEGRGNVPVQOYLMEKGSVPLKWTQESALIFPLNKSQDSGTGCT 300
 241 PPHREGOKLLHCEGRGNVPVQOYLMEKGSVPLKWTQESALIFPLNKSQDSGTGCT 300
 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHK 360
 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHK 360
 361 TYLTHEAKGSDADADATTAIINAEAGGSGGDDKEYFI 398
 361 TYLTHEAKGSDADADATTAIINAEAGGSGGDDKEYFI 398

RESULT 4
 AAY94403
 ID AAY94403 standard; protein; 398 AA.
 XX AAY94403;
 XX
 DT 11-SEP-2000 (first entry)
 DE Human ACAM cellular adhesion molecule encoded by cDNA clone ACAM#4.
 XX

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity or other activities. (Updated on 25-MAR-2003 to correct PR
 CC field.)

SQ Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCAWPGGANLSQDSDPWTSDTAVAGTVVLKQVKDHEDSSL 60
 DB 1 MGAPAAASLLLLLFFACCAWPGGANLSQDSDPWTSDTAVAGTVVLKQVKDHEDSSL 60

QY 61 QWSNPAQOTLYFGEKRALDNRNQLVSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDNRNQLVSTPHELSSISNVALADGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180

QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTQRIEVLVYTPPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTQRIEVLVYTPPTAMIRPD 240

QY 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPPFLNKSDSGTYGCT 300
 DB 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDPSPVSSSTVHAITGGIVAFIVFLLMLIFLGHYLRHKG 360
 DB 301 ATSNMGSKAYTYTLNVNDPSPVSSSTVHAITGGIVAFIVFLLMLIFLGHYLRHKG 360

RESULT 2

AA29592
 ID AAY29592 standard; protein; 398 AA.

AC AAY29592;

XX 14-OCT-1999 (first entry)

DT Human MBGP1 protein.

XX Human; MBGP1; therapy; diagnosis; immunoglobulin; multiple sclerosis;

KW cancer; neuronal disorder; CNS disorder; developmental disorder;

KW spinal injury; degenerative condition; viral infection; vaccine.

XX Homo sapiens.

OS EP939124-A2.

XX 01-SEP-1999.

XX 27-OCT-1998; 98EP-00203617.

XX 24-FEB-1998; 98GB-00003952.

PR 12-AUG-1998; 98GB-00017588.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Duckworth DM, Burgess NA;

PI WPI; 1999-480841/41.

DR N-PSDB; AAZ08540.

XX New immunoglobulin superfamily member, useful for diagnosing and treating

PT multiple sclerosis and cancer.

XX Claim 4; Page 17-18; 21pp; English.

CC The present sequence represents human MBGP1, which is a member of the
 CC immunoglobulin superfamily. MBGP1 may be used to screen for its agonists
 CC or antagonists by contacting MBGP1 with the candidate compound and
 CC detecting any alteration in activity of MBGP1 or in a label attached to
 CC the candidate. Alternatively the effect of a candidate agonist or
 CC antagonist compound on the production of mRNA encoding MBGP1 may be
 CC detected using an ELISA assay. Diseases or conditions arising from
 CC altered expression or activity of MBGP1 may be diagnosed by detecting
 CC MBGP1 in a sample from a patient or detecting a mutation in the
 CC polynucleotide encoding MBGP1 (I) in the genome of a patient. These
 CC diseases or conditions include neuronal disorders such as multiple
 CC sclerosis, CNS disorders, developmental disorders, spinal injury,
 CC degenerative conditions, cancer and viral infections. Detection of (I)
 CC may be used for chromosome mapping and tissue localization. MBGP1 and (I)
 CC may be administered to patients as vaccines or as part of a gene therapy
 CC regime respectively, to treat the diseases and conditions listed above.
 CC Antibodies against MBGP1 may be used to isolate or identify clones
 CC expressing MBGP1 or to purify MBGP1 by affinity chromatography. MBGP1 may
 CC also be used to identify molecules which interact with it in or on the
 CC surface of cells. Antagonists of MBGP1 may be administered to patients
 CC suffering from the above diseases or conditions related to increased
 CC expression or activity of MBGP1. Agonists of MBGP1 may similarly be used
 CC in cases of diseases or conditions related to decreased expression or
 CC activity of MBGP1

XX Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCAWPGGANLSQDSDPWTSDTAVAGTVVLKQVKDHEDSSL 60
 DB 1 MGAPAAASLLLLLFFACCAWPGGANLSQDSDPWTSDTAVAGTVVLKQVKDHEDSSL 60

QY 61 QWSNPAQOTLYFGEKRALDNRNQLVSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDNRNQLVSTPHELSSISNVALADGEYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180

QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTQRIEVLVYTPPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTQRIEVLVYTPPTAMIRPD 240

QY 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPPFLNKSDSGTYGCT 300
 DB 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPPFLNKSDSGTYGCT 300

QY 301 ATSNMGSKAYTYTLNVNDPSPVSSSTVHAITGGIVAFIVFLLMLIFLGHYLRHKG 360
 DB 301 ATSNMGSKAYTYTLNVNDPSPVSSSTVHAITGGIVAFIVFLLMLIFLGHYLRHKG 360

QY 361 TYLTHEAKSGDDPADTATINAEQGSGGDDKKKEYFI 398
 DB 361 TYLTHEAKSGDDPADTATINAEQGSGGDDKKKEYFI 398

RESULT 3

AA29592
 ID AAY13358 standard; protein; 398 AA.

AC AAY13358;

XX 25-JUN-1999 (first entry)

DE Amino acid sequence of protein PRO258.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 45.5528 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title: US-09-778-187b-10

Perfect score: 2086

Sequence: 1 MGAPAAALLLLLLPACCA.....AIIAEGGQSGDDKKEYFI 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2086	100.0	398	2 AAW80405	A secretes
2	2086	100.0	398	2 AAY29592	Human MBG
3	2086	100.0	398	2 AAY13358	Amino aci
4	2086	100.0	398	3 AAY94403	Human ACA
5	2086	100.0	398	3 AAY69288	Amino aci
6	2086	100.0	398	3 AAY45095	Human LDC
7	2086	100.0	398	3 ADC78404	Human PRO
8	2086	100.0	398	4 AAB80226	Human PRO
9	2086	100.0	398	4 AAU12345	Human PRO
10	2086	100.0	398	4 AAB53083	Human ang
11	2086	100.0	398	5 ABB84838	Human PRO
12	2086	100.0	398	5 ABB95444	Human arg
13	2086	100.0	398	5 ABP61823	Human pol
14	2086	100.0	398	6 ABU71604	Human PRO
15	2086	100.0	398	6 ABO17789	Novel hum
16	2086	100.0	398	6 ABU71459	Human PRO
17	2086	100.0	398	6 ABU81043	Human PRO
18	2086	100.0	398	6 ABU71905	Human sec
19	2086	100.0	398	6 ABO01788	Novel hum
20	2086	100.0	398	6 ABU66743	Human PRO
21	2086	100.0	398	6 ABU54361	Human PRO
22	2086	100.0	398	6 ABO47376	Human sec
23	2086	100.0	398	6 ABU59824	Novel sec
24	2086	100.0	398	6 ABO25014	Human sec
25	2086	100.0	398	6 ABU64513	Human sec

26	2086	100.0	398	6 ABU67359	Human sec
27	2086	100.0	398	6 ABO14879	Human sec
28	2086	100.0	398	6 ABU67019	Human sec
29	2086	100.0	398	6 ABU69636	Novel hum
30	2086	100.0	398	6 ABO14818	Human sec
31	2086	100.0	398	6 ADA45867	Novel hum
32	2086	100.0	398	6 ADA76298	Human PRO
33	2086	100.0	398	6 ADB29289	Human sec
34	2086	100.0	398	6 ADA18948	Human PRO
35	2086	100.0	398	6 ADA61571	Homo sapi
36	2086	100.0	398	6 ADB19356	Novel hum
37	2086	100.0	398	6 ADB27897	Human PRO
38	2086	100.0	398	6 ADA86376	Novel hum
39	2086	100.0	398	6 ADB15940	Human PRO
40	2086	100.0	398	6 ADA47726	Human PRO
41	2086	100.0	398	6 ADA18145	Human sec
42	2086	100.0	398	6 ABO32770	Human sec
43	2086	100.0	398	6 ADA67521	Human PRO
44	2086	100.0	398	6 ADB30528	Human PRO
45	2086	100.0	398	6 ADA85824	Novel hum

ALIGNMENTS

RESULT 1

AAW80405

ID AAW80405 standard; protein; 398 AA.

XX AC AAW80405;

XX DT 25-MAR-2003 (revised)

DT 13-JAN-1999 (first entry)

XX DE A secreted protein encoded by clone cr1162_25.

XX KW Secreted protein; immune stimulating; suppressing;

KW haematopoiesis regulating activity; tissue growth activity; activin;

KW inhibin activity; chemotactic; chemokinetic activity; haemostatic;

KW thrombolytic activity; anti-inflammatory activity; cadherin;

KW tumour invasion suppressor activity; tumour inhibition activity.

XX OS Homo sapiens.

XX PN WO9844113-A1.

XX PD 08-OCT-1998.

XX PF 27-MAR-1998; 98WO-US006176.

XX PR 28-MAR-1997; 97US-00823330.

XX PR 25-MAR-1998; 98US-00047661.

XX PA (GEMY) GENETICS INST INC.

XX PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

XX DR WPI: 1998-542703/46.

XX DR N-PSDB; AAV63189.

XX PT New isolated polynucleotide(s) and secreted proteins - are obtained from

PT human cDNA libraries prepared from adult testes, foetal brain, adult

XX brain, adult blood and placenta.

XX PS Claim 13; Page 70-71; 124pp; English.

XX CC The present sequence represents a secreted protein. The nucleic acid

CC sequence is isolated from a human adult testes cDNA library using probe

CC AAV63200. The polypeptide may have biological activities such as e.g.

CC nutritional activity, immune stimulating or suppressing activity,

CC haematopoiesis regulating activity, tissue growth activity,

CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

DR MGD; MGI:1889272; IgSF4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0018347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 35.3%; Score 736.5; DB 11; Length 445;
Best Local Similarity 38.4%; Pred. No. 1.4e-54;
Matches 163; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 9 LLLLLLPACCAFGANLSODSQPWTSDTVVAGGTIVLKCOVKDHDSSSLQWSNPAQQ 68
DB 31 LLLLLLSAALIFTG-----DQQLFTKDVTVIEGEVATISQVKNKSDSVIQLLNPNRQ 95

QY 69 TLYFGEKRALRDNRIOLVTSITPHELSSISNVALADEGYTCSIFTMPVRTAKSLVTVLG 128
DB 86 TIVFRDRLPKDSRFQLNPSSELKVLNVSISDEGRYFCQLYTDPPQESYTTITVLV 145

QY 129 IPQKPIITGYKSLREKDYATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKTF 188
DB 146 PPRNLMDIQDPAVEGEIEVNCATAMASKPATTIIRFKGNKELGK-SEVEEWS--MY 202

QY 189 TVSSSVTFQVTRDDGASIVCSVNHESLGADRSTSORIEVLVYPTAMIRPDPP---HPR 245
DB 203 TVTSQLMLKVHKEDDGVVICQVEHPAVTG-NLQTORYLEVQYKQVHIQMTYFLOGLTR 261

QY 246 EGOKLLHCEGRGNVPVQQYLWEK-EGSVPLPKMTQESALIFPFLNKSDSGTYGCTATSN 304
DB 262 EGDAPFELTCEAIGKQPQVVMVTVRVDDMEPQHAVLSGPNLFINLNKTDNGTYRCEASNI 321

QY 305 MGSYKAYYTLNVNDPS---PVPSSSTY-----HAITG 334
DB 322 VGKAHSDYMLYVYDPTTIPPPPTTTTITTTTTSILTIITDSRAGEEGTIGAVDHAVIG 381

QY 335 GIVAFIVFLLLIMLIFLGHYLIIRHKGYLTAEKGSDDAPDADTAIINAEQGSGGDDKK 394
DB 382 GVAVVVVFAMCLLIILGRYFAHKGYTFTEAKGADDAADADTAIINAEQGQNNSEKK 441

QY 395 EYFI 398
DB 442 EYFI 445

Search completed: May 27, 2004, 09:34:58
Job time : 33.6383 secs

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK001560; BAA91756.1; --
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003595; Neurexin-like.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Hypothetical protein; Immunoglobulin domain.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 163 AA; 17860 MW; FB746375A05B0006 CRC64;

Query Match 41.8%; Score 872; DB 4; Length 163;
 Best Local Similarity 100.0%; Pred. No. 7.9e-67;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSG 295

Db 1 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSG 60

QY 296 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYL 355

Db 61 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYL 120

QY 356 IRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398

Db 121 IRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 163

RESULT 13

QKLIH8 PRELIMINARY; PRT; 163 AA.

AC Q8KLIH8

DT 01-OCT-2002 (TREMELrel. 22, Created)

DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Similar to hypothetical protein FLJ10698.

GN NECL1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029659; AAH29659.1; --

DR MGD; MGI:2137858; Necl1.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

KW Hypothetical protein; Immunoglobulin domain.

SQ SEQUENCE 163 AA; 17773 MW; 1DBA707A03B71BBA CRC64;

Query Match 39.8%; Score 831; DB 11; Length 163;
 Best Local Similarity 95.1%; Pred. No. 2.6e-63;
 Matches 155; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 236 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSG 295

Db 1 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSG 60

QY 296 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYL 355

Db 61 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYL 120

QY 356 IRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398

Db 121 IRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 163

Db 121 IRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 163

RESULT 14

Q8BSQ8 PRELIMINARY; PRT; 152 AA.

ID Q8BSQ8

AC Q8BSQ8

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Nectin-like 1 (Fragment).

GN NECL1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Body;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs";

RL Nature 420:563-573 (2002).

DR EMBL; AK030782; BAC27137.1; --

DR MGD; MGI:2137858; Necl1.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

FT NON TER 1

SQ SEQUENCE 152 AA; 16458 MW; E41F6BAD6A413A7 CRC64;

Query Match 37.2%; Score 777; DB 11; Length 152;

Best Local Similarity 96.1%; Pred. No. 1e-56;

Matches 146; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 247 GQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSGTATSNMG 306

Db 1 GQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFFLNKS DSGTATSNMG 60

QY 307 SYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYLIRHKGYTLTHE 366

Db 61 SYKAYITLVNDPSPVSSSTYHAIIGGIVAFVFLLLIMLIFLGHYLIRHKGYTLTHE 120

QY 367 AKGSDPADADTAIINAEQSGGDDKKEYFI 398

Db 121 AKGSDPADADTAIINAEQSGGDDKKEYFI 152

RESULT 15

Q8K3T6 PRELIMINARY; PRT; 445 AA.

ID Q8K3T6

AC Q8K3T6

DT 01-OCT-2002 (TREMELrel. 22, Created)

DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Synaptic cell adhesion molecule 1.

GN IGSF4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL;

RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,

RA Sudhof T.C.;

RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly.;"

RL Science 0:0-0(2002)

DR EMBL; AF539424; AAN01614.1; --

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AC Q8N3J6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKF2P761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue Amygdala;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -
DR InterPro; IPR003599; IG
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein, Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 48.6%; Score 1014; DB 4; Length 435;
Best Local Similarity 47.2%; Pred. No. 2.1e-78;
Matches 204; Conservative 73; Mismatches 107; Indels 48; Gaps 6;

QY 11 LLLLFACWAPGANLSQDSQ--PWTSDETVVAGTVVLKCKQVHEDSSLOWNSPAQOT 69
DB 8 VLFYFVVC-----GLLQSGQGQFPFLTQNTVVEGGTALTTCRVDQNDNTSLOWNSPAQOT 63
QY 70 LYFGEKRALDRNRIQLVSTPHLSISGNVALADGEYTCSTFTMPVRTAKSLVTLGI 129
DB 64 LVPDDKALDRNRIELVRASWHELSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGV 123
QY 130 PKPIITGYKSSIREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKTTT 189
DB 124 PEKPIQSGFSSPWEGLMQLTCKTSGSKPAADIRWFKNDEIKDVKYLKEDANKTTT 183
QY 190 VSSVTFQVTRDDGASIVCSNVHESLKGADRTSQRIEVLVYPTAMIRPDPPHREGQK 249
DB 184 VSSLTDFRDRSDGVAICRVDPHESLNATPQVAMQVLEIHYTPSVKIIIPSTFPFQEQP 243
QY 250 LILHCEGRGNPVPQQYLWEKGSV---PPLKMTQESALIPFPFNKSDSGTYGCTATSNMG 306
DB 244 LIITCSKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNLFLNKTDNGTYRCEATNTIG 303
QY 307 SYKAYTYTLNVND-----PSPV-----PSSSSTV----- 329
DB 304 QSSAEVLIHVDPNTLLPTIIPSLTATVTTVAITTSPTTSATTSSIRDNPALAGQN 363
QY 330 ---HAITGGVAFIVFLLMLPLGHLRHKGYTLTHKAGSDADPADDTALINAEGB 386
DB 364 GPDHALIGGIVAVVVFVTLCSIFLLGRLYLRHKGYTLTHKAGSDADPADDTALINAEGB 423
QY 387 QSGGDDKKEYFI 398
DB 424 QVNAEKKKEYFI 435

RESULT 11
Q8IZP8 ID Q8IZP8 PRELIMINARY; PRT; 437 AA.
AC Q8IZP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
AFS38973; AAN16388.1; -
InterPro; IPR003599; IG
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_c2.
Pfam; PF00047; IG; 3.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 48.6%; Score 1013.5; DB 4; Length 437;
Best Local Similarity 47.1%; Pred. No. 2.3e-78;
Matches 206; Conservative 75; Mismatches 107; Indels 49; Gaps 7;

QY 11 LLLLFAC--CWAPGANLSQ--DSDQ---PWTSDETVVAGTVVLKCKQVHEDSSLOWNS 64
DB 1 MFVFLCNLSLVPAASAKNKVKGSQGFPLTQNTVVEGGTALTTCRVDQNDNTSLOWNS 60
QY 65 PAQOTLYFGEKRALDRNRIQLVSTPHLSISGNVALADGEYTCSTFTMPVRTAKSLV 124
DB 61 PAQOTLYFDDKKALDRNRIELVRASWHELSISVSDVSLSDGQYTCSLFTMPVKTSKAYL 120
QY 125 TVLGIPIQPIITGYKSSIREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPN 184
DB 121 TVLGVPEKPIQSGFSSPWEGLMQLTCKTSGSKPAADIRWFKNDEIKDVKYLKEDAN 180
QY 185 GKTFTVSSVTFQVTRDDGASIVCSNVHESLKGADRTSQRIEVLVYPTAMIRPDPPH 244
DB 181 RKTFTVSSLTDFRDRSDGVAICRVDPHESLNATPQVAMQVLEIHYTPSVKIIIPSTFP 240
QY 245 REGQKLLHCEGRGNPVPQQYLWEKGSV---PPLKMTQESALIPFPFNKSDSGTYGCTA 301
DB 241 QSGQPLIITCSKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNLFLNKTDNGTYRCEA 300
QY 302 TSNMGSYKAYTYTLNVND-----PSPV-----PSSSSTV----- 329
DB 301 TWITQSSAEVLIHVDPNTLLPTIIPSLTATVTTVAITTSPTTSATTSSIRDNPNA 360
QY 330 -----HAITGGVAFIVFLLMLPLGHLRHKGYTLTHKAGSDADPADDTAL 381
DB 361 LAGQNGPDHALIGGIVAVVVFVTLCSIFLLGRLYLRHKGYTLTHKAGSDADPADDTALI 420
QY 382 NAEQGGSGGDDKKEYFI 398
DB 421 NAEQGVNAEKKKEYFI 437

RESULT 12
Q9NVJ5 ID Q9NVJ5 PRELIMINARY; PRT; 163 AA.
AC Q9NVJ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ10698.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoaka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
Masubo Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
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Db 304 QSSAEYVLIVHDPNSLAGQDPHALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNE 363
QY 367 AKGSDADPADTAINAEGGQSGDDKKEYFI 398
Db 364 AKGAEDAPDADTAINAEGSQVNAEEKKEYFI 395
RESULT 8
Q8BYPI PRELIMINARY; PRT; 404 AA.
AC Q8BYPI1;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK038842; BAC30148.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG-LIKE; 3.
SQ SEQUENCE 404 AA; 44387 MW; E9C84191AA687473 CRC64;
Query Match 49.7%; Score 1037.5; DB 11; Length 404;
Best Local Similarity 53.1%; Pred. No. 1.8e-80;
Matches 196; Conservative 68; Mismatches 102; Indels 3; Gaps 1;
QY 33 PWTSDTVVAGGVTLVKCOVKDHESSLOWSPAAQOTLYFEGEKALRDNRILQVSTPHE 92
Db 36 PLTQNVTVVEGGTALTTCRVQNDNTSLQWSPAAQOTLYFDDKKALRDNRIELVRASWHE 95
QY 93 LSTISNVALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 152
Db 96 LSTISVDSVLSDEGGYTCSTFTMPVTKSKAYLTVLGVPEKPOISGFSSPVMEGDLMLTLC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVSSSVTFQVTRDDGASIVCSVN 212
Db 156 KTSQSKPAADIRFKNDKEIKDVYLKEEDANRKTFTVSTLDFRVDSDGVAVICRDV 215
QY 213 HESLKGADSTSRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQVYLWEKGS 272
Db 216 HESLNATPQVAMQVLEIHTPSVKIIPSTFPFQEGQALTLCESKGPPEPVLWTKGA 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTGYCTATSNMGSKAYVTLNVDPSVPSSSSTY 329
Db 276 ELPPDRMVVSGRELNLFLNKTDNGTYRCAETNTIGQSSAEVYLIVHDPNSLAGQNGPD 335
QY 330 HALIGGIVAFIVFLLLMIFLGHYLRHKGYLTNEAKGSDPADADTAINAEGGQSG 389
Db 336 HALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNEAKGAEDAPDADTAINAEGSQVN 395
QY 390 GDDKKEYFI 398
Db 396 AEEKKEYFI 404
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RESULT 10
Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
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RESULT 9
Q8BLQ9 PRELIMINARY; PRT; 404 AA.
AC Q8BLQ9;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK043760; BAC31646.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003989; VCM-1.
DR Pfam; PF00047; IG_3.
DR PRINTS; PRO1474; VCM1.
DR SMART; SM00409; IG_2.
DR SMART; SM00408; IG_c2; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
SQ SEQUENCE 404 AA; 44388 MW; 091E493B82CAFE5B CRC64;
Query Match 49.7%; Score 1037.5; DB 11; Length 404;
Best Local Similarity 53.1%; Pred. No. 1.8e-80;
Matches 196; Conservative 68; Mismatches 102; Indels 3; Gaps 1;
QY 33 PWTSDTVVAGGVTLVKCOVKDHESSLOWSPAAQOTLYFEGEKALRDNRILQVSTPHE 92
Db 36 PLTQNVTVVEGGTALTTCRVQNDNTSLQWSPAAQOTLYFDDKKALRDNRIELVRASWHE 95
QY 93 LSTISNVALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 152
Db 96 LSTISVDSVLSDEGGYTCSTFTMPVTKSKAYLTVLGVPEKPOISGFSSPVMEGDLMLTLC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVSSSVTFQVTRDDGASIVCSVN 212
Db 156 KTSQSKPAADIRFKNDKEIKDVYLKEEDANRKTFTVSTLDFRVDSDGVAVICRDV 215
QY 213 HESLKGADSTSRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQVYLWEKGS 272
Db 216 HESLNATPQVAMQVLEIHTPSVKIIPSTFPFQEGQALTLCESKGPPEPVLWTKGA 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTGYCTATSNMGSKAYVTLNVDPSVPSSSSTY 329
Db 276 ELPPDRMVVSGRELNLFLNKTDNGTYRCAETNTIGQSSAEVYLIVHDPNSLAGQNGPD 335
QY 330 HALIGGIVAFIVFLLLMIFLGHYLRHKGYLTNEAKGSDPADADTAINAEGGQSG 389
Db 336 HALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNEAKGAEDAPDADTAINAEGSQVN 395
QY 390 GDDKKEYFI 398
Db 396 AEEKKEYFI 404
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QY 121 KSLATVILGIPQPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGBPTRIQ 180
DB 121 KSLATVILGIPQPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGBPTRIQ 180
QY 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHSKLGADRSQTSQRIEVLVYPTTAMIRPD 240
DB 181 EDPND-----TPTAMIRPD 194
QY 241 PHPREGQKLLHCBGRGNVPQOVLWEKSGVPLKMTQ 280
DB 195 PHPREGQKLLHCBGRGNVPQOVLWEKSGVPLKMTQ 234

RESULT 6
Q8BZP4 PRELIMINARY; PRT; 395 AA.
ID Q8BZP4;
AC Q8BZP4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK033973; BAC28533.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG.c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; ig.3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG.2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 395 AA; 43516 MW; EB70FB5363D872F3 CRC64;

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Query Match 49.8%; Score 1039; DB 11; Length 395;
Best Local Similarity 51.3%; Pred. No. 1.3e-80;
Matches 201; Conservative 71; Mismatches 112; Indels 8; Gaps 3;

QY 11 LLLFACWAPGAGNLSQDSDQ-PWTSDETVVAGTVVLKQVKDHEDSSLOWNSPAQQT 69
DB 8 VLRFYSVC-----GLLQSGSQGQFPLTQNTVTVVGGTALTLCRVQDNDNTSLQNSPAQQT 63

QY 70 LYFGEKRALRDNRILQVLTSTPHELSSISINVALADEGETCSIFTMPVYRTAKSLVTLGI 129
DB 64 LYFDDKALRDNRILVRSWHELSSISVSDVSLSDGQYTCSLFTMPVYRTAKSLVTLGI 123

QY 130 POKPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGBPTRIQEDPNKGTFT 189
DB 124 PEKPIISGSPVMEGDLMLQTLCTSSGSKPAADIRWFKNDKEIKDVYKLEEADNRKFTT 183

QY 190 VSSSVTFQVTRDDGASIVCSVNHSKLGADRSQTSQRIEVLVYPTTAMIRPDPPHREGQK 249
DB 184 VSSLDFVRDSDGVAICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTFPQEQGA 243

QY 250 LLLHCBGRGNVPQOVLWEKSGV---PPLKMTQESALIPFPINKSDSGTYGCTATSNMG 306
DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRVMVSGRELNITFLNKTONGTYRCEATNTIG 303

QY 307 SYKAYTILNVNDSPVPSSSTVHAIIIGGVAFIVFLLIMLIFLGHYLRHKGYLTHTHE 366
DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRVMVSGRELNITFLNKTONGTYRCEATNTIG 303

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QY 307 SYKAYTILNVNDSPVPSSSTVHAIIIGGVAFIVFLLIMLIFLGHYLRHKGYLTHTHE 366
DB 304 QSSAKYVLIHDPNSLAGQGPDHALLIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNE 363
QY 367 AKGSDDAPDADTAIINAEAGGSGGDDKKEYFI 398
DB 364 AKGAEDAPDADTAIINAEAGSQVNAEKKKEYFI 395

RESULT 7
Q8BXJ7 PRELIMINARY; PRT; 395 AA.
ID Q8BXJ7;
AC Q8BXJ7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK046800; BAC32876.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG.c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; ig.3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG.2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 395 AA; 43517 MW; E57E1BBD6D3672F9 CRC64;

```

```

Query Match 49.8%; Score 1039; DB 11; Length 395;
Best Local Similarity 51.3%; Pred. No. 1.3e-80;
Matches 201; Conservative 71; Mismatches 112; Indels 8; Gaps 3;

QY 11 LLLFACWAPGAGNLSQDSDQ-PWTSDETVVAGTVVLKQVKDHEDSSLOWNSPAQQT 69
DB 8 VLRFYSVC-----GLLQSGSQGQFPLTQNTVTVVGGTALTLCRVQDNDNTSLQNSPAQQT 63

QY 70 LYFGEKRALRDNRILQVLTSTPHELSSISINVALADEGETCSIFTMPVYRTAKSLVTLGI 129
DB 64 LYFDDKALRDNRILVRSWHELSSISVSDVSLSDGQYTCSLFTMPVYRTAKSLVTLGI 123

QY 130 POKPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGBPTRIQEDPNKGTFT 189
DB 124 PEKPIISGSPVMEGDLMLQTLCTSSGSKPAADIRWFKNDKEIKDVYKLEEADNRKFTT 183

QY 190 VSSSVTFQVTRDDGASIVCSVNHSKLGADRSQTSQRIEVLVYPTTAMIRPDPPHREGQK 249
DB 184 VSSLDFVRDSDGVAICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTFPQEQGA 243

QY 250 LLLHCBGRGNVPQOVLWEKSGV---PPLKMTQESALIPFPINKSDSGTYGCTATSNMG 306
DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRVMVSGRELNITFLNKTONGTYRCEATNTIG 303

QY 307 SYKAYTILNVNDSPVPSSSTVHAIIIGGVAFIVFLLIMLIFLGHYLRHKGYLTHTHE 366
DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRVMVSGRELNITFLNKTONGTYRCEATNTIG 303

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SEQUENCE 394 AA: 42730 MW: F1141D8E6B69254A CRC64:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 32.6383 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPASALLLLLLLAFACWA.....AIIAAGSGSGGDKKEYFI 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	398	4 Q8N126	Q8N126 homo sapien
2	2059	98.7	432	4 Q9UJP1	Q9UJP1 homo sapien
3	1970	94.4	396	11 Q9N28	Q9N28 mus musculus
4	1282.5	61.5	394	13 Q7ZXX1	Q7ZXX1 xenopus lae
5	1203	57.7	234	4 Q81ZQ9	Q81ZQ9 homo sapien
6	1039	49.8	395	11 Q8BZP4	Q8BZP4 mus musculus
7	1039	49.8	395	11 Q8BXJ7	Q8BXJ7 mus musculus
8	1037.5	49.7	404	11 Q8BYP1	Q8BYP1 mus musculus
9	1037.5	49.7	404	11 Q8BLQ9	Q8BLQ9 mus musculus
10	1014	48.6	435	4 Q8N3J6	Q8N3J6 homo sapien
11	1013.5	48.6	437	4 Q81ZP8	Q81ZP8 homo sapien
12	872	41.8	163	4 Q9NVJ5	Q9NVJ5 homo sapien
13	831	39.8	163	11 Q8K1H8	Q8K1H8 mus musculus
14	777	37.2	152	11 Q8BSQ8	Q8BSQ8 mus musculus
15	736.5	35.3	445	11 Q8K3T6	Q8K3T6 mus musculus
16	736.5	35.3	445	11 Q8R4L1	Q8R4L1 mus musculus

17	736	35.3	442	4 Q9BY67	Q9BY67 homo sapien
18	727.5	34.9	417	11 Q7TNL1	Q7TNL1 mus musculus
19	726	34.8	456	11 Q8R5M8	Q8R5M8 mus musculus
20	724.5	34.7	443	4 Q8N2F4	Q8N2F4 homo sapien
21	607	28.1	388	4 Q8NFZ8	Q8NFZ8 homo sapien
22	598	28.7	388	11 Q8R464	Q8R464 mus musculus
23	573.5	27.5	381	4 Q9Y4A4	Q9Y4A4 homo sapien
24	514	24.6	295	11 Q9QYL6	Q9QYL6 mus musculus
25	510	24.4	295	11 Q9Z2H8	Q9Z2H8 mus musculus
26	508.5	24.4	306	11 Q9QYL4	Q9QYL4 mus musculus
27	503.5	24.1	278	11 Q9QYL3	Q9QYL3 mus musculus
28	499	23.9	289	11 Q9QYL5	Q9QYL5 mus musculus
29	474	22.7	333	4 Q86WB8	Q86WB8 homo sapien
30	471.5	22.6	336	11 Q9D6E7	Q9D6E7 mus musculus
31	471.5	22.6	336	11 Q80VG4	Q80VG4 mus musculus
32	345.5	16.6	403	6 Q8HY15	Q8HY15 lemur catta
33	307	14.7	412	6 Q8HY14	Q8HY14 cryptotagus
34	290	13.9	401	6 Q88835	Q88835 cercopithec
35	281	13.5	417	4 Q96BJ1	Q96BJ1 homo sapien
36	273	13.1	612	11 Q8BQG5	Q8BQG5 mus musculus
37	273	13.1	766	11 Q81OH3	Q81OH3 mus musculus
38	273	13.1	778	11 Q8BR86	Q8BR86 mus musculus
39	271	13.0	778	4 Q8IZU9	Q8IZU9 homo sapien
40	271	13.0	779	4 Q96JG0	Q96JG0 homo sapien
41	258.5	12.4	439	13 Q57349	Q57349 gallus gall
42	254	12.2	412	11 Q63611	Q63611 rattus norv
43	254	12.2	412	11 Q9R1E1	Q9R1E1 rattus norv
44	252.5	12.1	393	4 Q95727	Q95727 homo sapien
45	252	12.1	350	7 Q02869	Q02869 gallus gall

ALIGNMENTS

RESULT 1

Q8N126	Q8N126	PRELIMINARY;	PRT;	398 AA.
AC	Q8N126;			
DT	01-OCT-2002 (T-EMBLrel. 22, Created)			
DT	01-OCT-2002 (T-EMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)			
DE	Brain immunoglobulin receptor precursor (Nectin-like protein 1)			
DE	(TSLC1-like 1).			
GN	TSL1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Cunningham S.A., Tran T.M., Arrate M.P.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Strausberg R.;			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Fukuhara H., Murakami Y.;			
RT	*Isolation of the TSL1 and TSL2 genes, members of the tumor			
RT	suppressor TSLC1 gene family encoding transmembrane proteins.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY046418; AAL02143.1; -			
DR	EMBL; E033819; AAL03819.1; -			
DR	EMBL; AF363367; AAM60749.1; -			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF000047; ig; 3			
DR	SMART; SM00409; IG; 3.			

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FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 258 258 N -> S.
/FTIG=VAR_003907.
M -> T.
/FTID=VAR_003908.

FT VARIANT 301 301
FT STRAND 32 33
FT STRAND 39 44
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 71
FT STRAND 76 78
FT TURN 84 85
FT STRAND 86 90
FT STRAND 95 100
FT STRAND 110 117
FT TURN 118 119
FT STRAND 120 123
FT STRAND 127 128
FT STRAND 130 131
SQ SEQUENCE 583 AA; E023FB3974A60284 CRC64;

Query Match 10.8%; Score 225.5; DB 1; Length 583;
Best Local Similarity 22.4%; Pred.No. 7.8e-09;
Matches 80; Conservative 70; Mismatches 148; Indels 59; Gaps 14;

QY 2 GAPAASILLLLLPACQWAPGGANLSQDDSQPWTSDETVVGTVLKCQVK----- 53
Db 5 GASSCRLLFCLLISATVFRG-----LGYTVNSAY-GDTIIIPCRLDVPQNLMSG 54
QY 54 -----DHEDSS---LQSNPAQOTLYFGEKRALRDNRILQVTSTPHELSTISINVALADEG 106
Db 55 KWKYKPDGSPVFIAFRSSTKSKVQDDVPEYKD-RLNL-----SENYTLSISNARISDEK 109
QY 107 EYTCSTFTMP-VRTAKSLVTLGIPQKPIITGYKSSLRKXDATL-NCQSSGSKPAARLT 164
Db 110 RFVCMVLVEDNVFEAPTIVKVFQKPSKPEIVSKALFLETEQLKXGDCISEDSYPDGNIT 169
QY 165 WRKGDQELH---GEPTRI---QEDPGKTFVSSSVTFQVTRDDGASIVCSVSNHESLKG 218
Db 170 WYRNGKVLHLEAGVAVIIFKEMDPVTLQYTMSTLEYKTKKADIQMPFTCSVTYYGPSG 229
QY 219 ADR-STSQRIEIVTPTAMIR-----PDPPHREGQKLLHCEGRGNVPQOYLWEKEGSV 273
Db 230 QKTHSEQAVEDIYYPTQVTVLPPKNAIKEGDNITLKLGNPNPPBEFLFYLPGQP 289
QY 274 PPLKMTQESALIFPLKNSDSTGYGCTATSNMGSYKAYITLVNDPSPVSSSTYH 330
Db 290 EGIRSSNTYTLN--DVRNATGDKCSU-----IDKSMIASTAITVH 330

Search completed: May 27, 2004, 09:35:46
Job time : 9.4531 secs
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FT SITE 432 435 SH2-BINDING (POTENTIAL) .
FT SITE 441 446 SH3-BINDING (POTENTIAL) .
FT SITE 455 458 SH2-BINDING (POTENTIAL) .
FT SITE 472 475 SH2-BINDING (POTENTIAL) .
FT SITE 498 501 SH2-BINDING (POTENTIAL) .
FT MOD_RES 431 431 PHOSPHORYLATION (BY TYR-KINASES)
(POTENTIAL) .
FT MOD_RES 455 455 PHOSPHORYLATION (BY TYR-KINASES)
(POTENTIAL) .
FT MOD_RES 472 472 PHOSPHORYLATION (BY TYR-KINASES) (BY
SIMILARITY) .
FT MOD_RES 498 498 PHOSPHORYLATION (BY TYR-KINASES) (BY
SIMILARITY) .
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT VARIANT 23 23 N -> S.
FT VARIANT 28 28 T -> A.
FT VARIANT 61 61 S -> L.
FT VARIANT 70 70 K -> R.
FT VARIANT 120 120 Y -> H.
FT VARIANT 125 125 R -> Q.
FT VARIANT 127 127 E -> G.
FT VARIANT 129 129 R -> H.
FT VARIANT 132 132 M -> V.
FT VARIANT 145 145 S -> N.
FT VARIANT 153 153 L -> V.
FT VARIANT 203 203 N -> D.
FT VARIANT 261 261 G -> R.
FT VARIANT 302 302 F -> L.
FT VARIANT 316 316 F -> L.
FT VARIANT 337 337 G -> R.
FT VARIANT 367 367 S -> N.
FT VARIANT 422 422 Q -> L.
FT VARIANT 429 429 I -> F.
FT VARIANT 433 433 D -> E.
SQ SEQUENCE 506 AA; 55093 MW; 6B7E310677FCF9CB CRC64;

Query Match 10.9%; Score 226.5; DB 1; Length 506;
Best Local Similarity 23.1%; Pred. No. 5.5e-09;
Matches 98; Conservative 69; Mismatches 184; Indels 73; Gaps 18;

Qy 8 LLLLLL FACWAGGANLSODDSOPWTSDETVVAGGVVLKCOVKDHD--SSLOW---S 63
Db 14 LCLLLAASNAWGTAGDELQVTPERS-VSVAAGETATLHCTVLSLSPGVPIKFKGT 72
Qy 64 NPAQITLYFGEKRALDRNRIRQLVSTPH---ELSGISINVALADEGYTCISFTMPVRTA 120
Db 73 GPGEFIY-SQKEAFPRFTVNTVSDATKRNWDFSRISNITPADAGVYCVKPKKEERG 131
Qy 121 KSL-----VTVLGIPQKPIITGYKSLRKBKOTATLNCQSSGSKPA-ARLTWRKQDQEL 172
Db 132 MEFGSGPGTHLTVSAKPPVLSGPTVRATPEQTVFTCTSHGFSRPNISLKNWFKNGNEL 191
Qy 173 HGEPTRIQEDNGKFTFTVSSVTVQVTRDDGASIVCSVNHESLKGAD--RSTSORLEVL 230
Db 192 SASQTSVDPENNVSYSINSTKVLATGVDHVSQVCEVAHVTLQGGPPLRGTLANLSETI 251
Qy 231 YTPATAMIRPDPPHREGQKLLHCE-GRGNFVPQOYLWEKEGSPPLKWTQESALIFPFL 289
Db 252 RVPPTL--EITGSPAGQNVNTCVNKFYRHLQLTLENGM-----SRTEASVFFV-- 303
Qy 290 NKDSGSGTYGCTATSNMGS-----YKAYYTLNVNDP-----SP 321

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Db 304 -ENKDGTFNQTSWFLVNSSAHREAVLTCQVHDQPAVSKNHTLEVSAPQKDQDTGTP 362
Qy 322 VPSS--STYHAITGGIVAFIVFILLIMLIFLGHVLIHKGTYLTHEAKGSDDA-----P 374
Db 363 GFNSDNWTSIFIVGVWCALLVALLAAL-----YLLRIR---QNKARGSTSTRLHP 413
Qy 375 DADT 378
Db 414 EKNT 417

RESULT 14
LAMP RAT STANDARD; PRT; 338 AA.
ID LAMP RAT
AC O62813.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Limbic system-associated membrane protein precursor (LSAMP) .
GN LSAMP OR LAMP.
OS Rattus norvegicus (Rat) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-49.
RC TISSUE=Hippocampus;
RX MEDLINE=95374785; PubMed=7646886;
RA Fimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
RA Hensel W., Fischer I., Levitt P.;
RT "The limbic system-associated membrane protein is an Ig superfamily
RT member that mediates selective neuronal growth and axon targeting.";
RL Neuron 15:287-297(1995).
CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
CC MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
CC OF THE HIPPOCAMPAL MOSSY FIBER PROJECTION.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic-
CC associated cortical and subcortical regions that function in
CC cognition, emotion, memory, and learning.
CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS
CC DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE
CC THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN
CC HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
CC REGION.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U31554; AAA86120.1; -.
CC InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003598; Ig_C2.
CC DR Pfam; PF00047; Ig; 3.
CC DR SMART; SM00408; IGC2; 2.
CC DR PROSITE; PS50835; IGLIKE; 3.
CC DR Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 28
FT CHAIN 29 315 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROPEP 316 338 REMOVED IN MATURE FORM (POTENTIAL) .
FT DOMAIN 29 122 IG-LIKE C2-TYPE 1.
FT DOMAIN 132 214 IG-LIKE C2-TYPE 2.

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FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SEQUENCE 583 AA; 65161 MW; E7BFAFC8F9489 CRC64;

Query Match
Best Local Similarity 11.0%; Score 228.5; DB 1; Length 583;
Matches 97; Conservative 55; Mismatches 159; Indels 99; Gaps 17;

QY 3 APAASILLILLFACCAWAGCANLSDQDQPTSDFTVAGGVVLKCVCKHEDSSLOW 62
DB 6 SPSCRIVFCLLSAAVLRPG-----LGWTVNSAY-GDTIVMPCLR----- 45
QY 63 SNAQQTLYFGEXR-----ALRDNRIQLV-----TSTPHELISISNV 100
DB 46 --DVPQNLMEGKKYKPKDPSVFIAFRSTKKSQVDDVPEVKDRLSLSENYTSLIANA 103
QY 101 ALADEGYTCISFTMP-VRTAKSLTVLGHIPQIPITIGYKSSREKDTATL-NCQSSGSK 158
DB 104 KISDEKRFVCLVTEDNVFEAPTLVKVFKQPSPEIVNKPAPLETDLQKLGDICISDSY 163
QY 159 PAARLTW-RKGD--OELHGEPT---RIOEDPNGKTFVTSSSVTFQVTRDDGASIVCSVN 212
DB 164 PDGNITWYRNGKVLQPVGEVAILFKEDIDFGQLYIVTSLSLEYKTRSDIQWFTCSVT 223
QY 213 HESLKGADRTS-QRIEVLTYPTAMIR-----PDPPHREGQKLLHCEGRGNVPVQOYLW 267
DB 224 YGSPSGQKTIYSQEIFDIYYPTEQVTIQVLPKNAIKEGDNITLQCLGNNGNPPPEFNF 283
QY 268 EKGSGVPLKMTQESALIFPLKNSDGTGCTATS--NMGSKYA-----YYTLNVN---- 317
DB 284 YLPQ--PEGIRSNNTYTLTDVRNATGDKYKSLIDKRNMAASTTIVHVHLDLSLNPRGE 341
QY 318 -----DPSPV-----PSSSTYHALIGIV 337
DB 342 VTKQIGDTLPSVCTISASRNATVVMKDNIRLSSPSFSLHYQDAGNYV 391

RESULT 12
PVR2 HUMAN STANDARD; PRT; 538 AA.
AC Q2692; Q75455; Q96729;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
DE mediator B) (HvEB) (Nectin 2) (CD112 antigen).
GN PVR2 OR PRR2 OR HVEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene
RT (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
RT susceptibility to infection by mutants of herpes simplex virus type
RT 1, herpes simplex virus type 2, and pseudorabies virus.";
RL Virology 246:179-189(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny E., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE OF 31-538 FROM N.A.
RA Yoshiura K., Murray J.C.;
RT "A transcriptional map in the region of 19q13 derived using direct
RT sequencing and exon trapping.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 449-538 FROM N.A.
RX MEDLINE=99449047; PubMed=10520737;
RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA Ashworth L.K., Van Bockmeer F.M., Dawkins R.L.;
RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
RL PEREC1.";
RL DNA Seq. 9:89-101(1998).
CC -!- FUNCTION: RECEPTOR FOR ALPHAPERPEVIRUS (HSV-1, HSV-2 AND
CC -!- PSEUDORABIES VIRUS); ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Delta;
CC IsoId=Q92692-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=PROV 1:74-77(2000);
CC WWW='http://www.ncbi.nlm.nih.gov/prov/guide/204270028_g.htm'.
CC -----
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CC -----
EMBL; X80038; CAA56342.1; -
EMBL; AF058448; AAC23797.1; -
EMBL; BC003091; AAH03091.1; -
EMBL; AF044968; AAC82348.1; -
EMBL; AF044962; AAC82348.1; JOINED.
EMBL; AF044963; AAC82348.1; JOINED.
EMBL; AF044964; AAC82348.1; JOINED.
EMBL; AF044966; AAC82348.1; JOINED.
EMBL; AF044967; AAC82348.1; JOINED.
EMBL; AF050154; AAD02503.1; -
PIR; I68093; I68093.
Gene; HGNC:9707; PVR2.
MIM; 600798; -
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0015026; F:coreceptor activity; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
Pfam; PF000047; Ig; 2.
SMART; SM00409; Ig; 1.
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FT DOMAIN 376 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 436 442 POLY-GLU.
FT DOMAIN 443 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 138 138 L -> P (IN REF. 1).
FT CONFLICT 165 165 N -> D (IN REF. 1).
FT CONFLICT 342 342 P -> PP (IN REF. 2).
FT CONFLICT 428 428 S -> G (IN REF. 3).
SQ SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;

Query Match 11.0%; Score 228.5; DB 1; Length 515;
Best Local Similarity 26.2%; Pred. No. 4e-09;
Matches 112; Conservative 59; Mismatches 153; Indels 103; Gaps 26;

QY 43 GTDWLKCQVKDEDS-----SLOW---SNPAQOTLYFGEKRALDRNRKIQLVTSPEL-- 93
Db 44 GTDVLHCFANPLPSVKITQVTWQASNGSKQNM-----ALYNTMGVSVLPPEKRV 97
QY 94 -----SISINVALADEGEYTCISPTMPVPTAKSLVTVLGIPOKPI--ITGXSS 141
Db 98 EFLRPSFIDGIRLGLLEDEGMYICEFATFPTGNRESQLN-LTWAKPTNWIETRAV 156
QY 142 LREK---DRTAL--NCOSSGSKPAARLTWRKQDELHGEPTRIQE--DPNGKFTVSSSV 194
Db 157 LRARKGDKNLVATCTSANGKPPSAVSW---ETRLKGE--AEYQEIERNPNG--TVTVISRY 211
QY 195 TFOVTRDDGASIVCSVNHSLKGAIR-STSQRIEVLVPTAMIRP--DPHPREGQKLIL 252
Db 212 RLVPSEARHQSLACIVNHY---LDRFRESLINVQYEPVETIRGFDGNWYLQRTDVKL 267
QY 253 HCEGRNPVQQLWEK-EGSVPLKMTQBSALIF--PFLNKSDSGTYGCTATSNNGSYK 309
Db 268 TKADANPATEYHYHTTLNGLSLPKGVEAQNRTLFFRGP-ITYSLAGTYICEATNPIGTRS 326
QY 310 AYTLANVD---PSP-----VPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHVLI- 356
Db 327 QQVEVITEFPYTPTEHGRRAQOMPT-----ALIGGVAGSV-----LLVLIIVGGIIVA 376
QY 357 ----RH--KGTYLT-----HEAKGSDADPADTATINAEQGQS 388
Db 377 LRRRRHTFGDSTKHHVYNGYSGKAGIQPHHPMAQNLQVPDSDDEKKA--SPLGSS 434
QY 389 GGDCKE 395
Db 435 YEEEEE 441

RESULT 11
ID C166_MOUSE STANDARD; PRT; 583 AA.
AC Q61490; Q70136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE ALCAM (DM-GRASP protein).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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RN RP SEQUENCE FROM N.A.
RC STRAIN=NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Agid M., Whitney G.S., Palmer D.,
RA Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs and mediates cross-species binding.";
RL Bur. J. Immunol. 27:1469-1478(1997).
RN RP SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse.";
RL J. Neurobiol. 25:831-845(1994).
CC -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC -----
DR EMBL; U95030; AAC06342.1; -
DR EMBL; L25274; AAA37528.1; -
DR HSSP; Q13740; 1KJC.
DR MGD; MGI:1313266; Alcam.
DR GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
DR GO; GO:0007165; P:signal transduction; IPI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 120 IG-LIKE V-TYPE 1.
FT DOMAIN 125 234 IG-LIKE V-TYPE 2.
FT DOMAIN 245 328 IG-LIKE C2-TYPE 1.
FT DOMAIN 333 409 IG-LIKE C2-TYPE 2.
FT DOMAIN 416 501 IG-LIKE C2-TYPE 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 334 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 227 232 PSQKQT -> AAGIPA (IN REF. 2).
```

RT anchored protein (Kilon), a member of the IgLON cell adhesion molecule family".; Chem. 274:8224-8230(1999).

CC -!- FUNCTION: CELL-ADHESION (POTENTIAL).

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: Highly expressed in brain.

CC -!- PTM: Glycosylated.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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DR EMBL: AB017139; BAA75649.1; -.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003598; Ig_c2.

DR Pfam: PF00047; Ig; 3.

DR SMART: SM00408; IGC2; 2.

DR PROSITE: PSS0835; IG_LIKE; 3.

KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;

KW Repeat; Signal.

FT SIGNAL 1 31 ? KILON PROTEIN.

FT CHAIN 32 ? REMOVED IN MATURE FORM (POTENTIAL).

FT PROPEP 32 348 IG-LIKE C2-TYPE 1.

FT DOMAIN 32 128 IG-LIKE C2-TYPE 2.

FT DOMAIN 133 215 IG-LIKE C2-TYPE 3.

FT DOMAIN 219 307 POTENTIAL.

FT DISULFID 54 112 POTENTIAL.

FT DISULFID 154 197 POTENTIAL.

FT DISULFID 239 291 POTENTIAL.

FT CARBOHYD 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 280 280 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 348 AA; 37858 MW; 37E90D1C7D24ACAB CRC64;

Query Match 11.2%; Score 233.5; DB 1; Length 348;

Best Local Similarity 24.8%; Pred. No. 1e-09;

Matches 82; Conservative 55; Mismatches 133; Indels 41; Gaps 13;

Qy 9 LLLLLLACWAPGAGNLSDSQPWTSDETVA--GGTVLKKQVKDHEEDSLQSNPA 66

Db 15 LAAVLLSLCCLPAG----QSVDFPMAAVDNMLVRKGTAVLRCLYLEDGA-SKGAWLNRS 69

Qy 67 QOTLYFCEKALRNRIQLVSTSTHELSISISYVALADEGEYTCISITMPVPTAKSLVTV 126

Db 70 SIIFAGGDKMSV-DPRVSIISLNRKDSIQNVDDVTDGYSVOTQHTPTPMQVHLT 128

Qy 127 LGIPKPKIITGYKSLREKDTATLNCSSGSKPAARLTWRKQDQLHGEPTRIQEDPENGK 186

Db 129 VQVPFKIYDINSDMTINEGTNVTITCLATG-KPEPAISWR-----HISPS-AKPFENGQ 180

Qy 187 TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYTPAM-IRPDPPHPR 245

Db 181 YLDI-----YGITRDQAGEYECSEANDVSFDDVKK--VRVVNFAPTIQIKSGTVTP- 231

Qy 246 EGQKLLHCEGRGNVP-----QVILWEKGSVPFLKMTQESALLFPFLNKSDSGTYG 298

Db 232 -GRSLIRCEGAGVPPPAFEWYKKEKRLFNQCQGIITQNFSTRSILVTNVTQEHFGNYT 290

Qy 299 CTATSNMGSKYKAYTLNVNDSPPVSSSTY 329

Db 291 CVAANKLGTWASLPLN-----PPSTAQY 314

RESULT 10

PVRL MOUSE

ID PVRL MOUSE STANDARD; PRT; 515 AA.

AC Q9JUF6; Q9ERL5; Q9JIL7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).

GN PVRL1 OR PVRL1 OR HVEC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2043787; PubMed=10781093;

RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Leccocq E., Dubreuil P., Campadelli-Fiume G.;

RT "The murine homolog of human nectin1 delta serves as a species non-specific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20541977; PubMed=11090177;

RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;

RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha (HvEC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";

RL J. Virol. 74:11773-11781(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Swiss Webster;

RA Zhan J., Wimmer E.;

RT "Mouse nectin-1 (mPR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RL -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.

CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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DR EMBL: AF239762; AAF60333.1; -.

DR EMBL: AF270977; AAF76195.1; -.

DR EMBL: AF297665; AAG22808.1; -.

DR MGD; MGI:1926483; Pvr11.

DR GO: GO:0005913; C:cell-cell adherens junction; IDA.

DR GO: GO:0005515; F:protein binding; IPI.

DR GO: GO:0004872; F:receptor activity; IDA.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003599; Ig.

DR Pfam: PF00047; Ig; 2.

DR SMART: SM00409; IG; 2.

DR PROSITE: PSS0835; IG_LIKE; 2.

KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

KW Repeat; Glycoprotein; Signal.

FT SIGNAL 1 30

FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.

FT DOMAIN 31 354 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 355 375 POTENTIAL.

QY 197 QVTREDDGASIVGVNHESLKGADR-STSORIEVLYTPTAMIRP-DPPHPREGQKLLHLC 254
 Db 214 VPSREAHQSLACIVNH---MDRFKESITLVNQVEPEVTIGFDGNWYLRMDVKLIC 269
 QY 255 EGRGNVPQOYLMEK-EGSVPPKMTQESALIPFF-LNKSDSTGYCTATSNMGSKAYY 312
 Db 270 KADANPPATEYHTWTLNGLSLPKGVEAQNRTLFFKGPINTYSLAGTYICEATNPITGRSGQV 329
 QY 313 TLNVND---PS-----PVPSSSTVHALIGGIVAFIVFLLIMLIFLGHYLI--- 356
 Db 330 EVNITFPYTPSPPEHRRAGPVPT-----ALIGGVAGSI-----LVLIVGGIVVALR 379
 QY 357 --RH--KGYLT-----HEAKGSDPADPADTATINAEQSGSG 390
 Db 380 RRHTFKGDYSTKHHVYNGVSKAGIPQHPHMAQNLQYDPDSDDEKKA--GPLGGSSYE 437
 QY 391 DDKE 395
 Db 438 EEEEE 442

RESULT 8

OPCM_CHICK STANDARD; PRT; 337 AA.
 AC Q98892;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Opioid binding protein/cell adhesion molecule homolog precursor
 DE (Neurite inhibitor GP55-A) (OBCAM protein gamma isoform).
 GN OPCML.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
 RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from
 RL chick: structural diversity of IGLON family proteins.";
 RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97157768; PubMed=9004047;
 RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
 RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
 RT are members of the Ig superfamily and are related to OBCAM,
 RT neurotrophin, LAMP and CEPU-1.";
 RL J. Cell Sci. 109:3129-3138(1996).
 CC -!- FUNCTION: Inhibits neurite outgrowth.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Restricted to the nervous system.
 CC -!- DEVELOPMENTAL STAGE: Increases during development from very low
 CC levels at embryonic day 10 and is most abundant after hatching.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC
 CC EMBL; Y08170; CAB41420.1; --
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; Ig; 3.

DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
 KW Membrane; GPI-anchor; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 314
 FT PROPEP 315 337
 FT DOMAIN 32 119
 FT DOMAIN 129 211
 FT DOMAIN 215 302
 FT DISULFID 50 108
 FT DISULFID 150 194
 FT DISULFID 236 288
 FT LIPID 314 314
 FT CARBOHYD 133 133
 FT CARBOHYD 277 277
 FT CARBOHYD 285 285
 FT CARBOHYD 298 298
 SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;
 Query Match 11.3%; Score 235.5; DB 1; Length 337;
 Best Local Similarity 25.3%; Pred. No. 7.2e-10;
 Matches 92; Conservative 58; Mismatches 151; Indels 63; Gaps 16;
 QY 18 CW-----APGGANLSQDSDSOPWTSDE-TVVAGGTVLKCOVKHEDSSLOWSNP 65
 Db 6 CWIVFTATTALLFIPGVPRSGDATPFKAMDNVTVQGESATLRCCTVDDV-RRVAWLN- 63
 QY 66 AQTLYFGEKRALRDNRIQLVTSPELHSSISNVALADEGYTCSIFTMPVRTAKSLVT 125
 Db 64 RSTLYAGNDKWSIDNRVILSKTKQYSIKIHNVVDYDEGPTCSVQTDNHPKTSRVL 123
 QY 126 VLGIPOKPIITGYKSSLRKDTATINCQSSGSKPAARLTWRKQDQELHGEPTIQEDP 185
 Db 124 IVQVPPQIVNISSDITVNEGSSVTLMLCLAFG-RPEPTVTWR-----HLSGK- 169
 QY 166 KTFVTSSSVTFQ---VTREDDGASIVGVNHESLKGADRSTSORIEVLYTPTAMIRPDP 242
 Db 170 QGF-VSEDEVLEITGTITREGSGEYECANVDVAVPVRK---VKVVNY-----PP 216
 QY 243 H-----PREQKLLHCEGRGNVPQOYLMEK-----GSVPLPKMTQE---SALIF 286
 Db 217 YISNAXNTGASVGQKGLQCEASAVPV-AEFQFKEDTRLANGLEGVRIESKGRSLTLTF 275
 QY 287 PFLNKSDSGTYGCTATSNMGSKAYYTLNVNDRSPVSSSTVHALIGGIVAFIVFLLI 346
 Db 276 FNVSEKDYGNVTCVATNKLGNATNA--SIILYGPVAVHDSGNAAASRAAGLCLWATLLAR 333
 QY 347 MLIF 350
 Db 334 LLDF 337
 RESULT 9
 KILO RAT
 ID KILO RAT STANDARD; PRT; 348 AA.
 AC Q920J8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kilon protein precursor (Kindred of IGLON).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
 RX MEDLINE=99175207; PubMed=10075727;
 RA Funatsu N., Miyata S., Kumanogoh H., Shigeta M., Hamada K., Endo Y.,
 RA Sokawa Y., Maekawa S.;
 RT "Characterization of a novel rat brain glycosylphosphatidylinositol-

RA Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B.
 RX MEDLINE=99401000; PubMed=10469599;
 RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
 RA Schraven B., Neel B.G.;
 RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
 RT multi-protein complexes in macrophages.";
 RL Curr. Biol. 9:927-930(1999).
 RN [8]
 RP PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH PTPN11 AND JAK2.
 RX MEDLINE=20428742; PubMed=10842184;
 RA Stofega M.R., Argentesinger L.S., Wang H., Ullrich A., Carter-Su C.;
 RT "Negative regulation of growth hormone receptor/JAK2 signaling by
 RT signal regulatory protein alpha.";
 RL J. Biol. Chem. 275:28222-28229(2000).
 RN [9]
 RP FUNCTION, AND INTERACTION WITH CD47.
 RX MEDLINE=21400825; PubMed=11509594;
 RA Latour S., Tanaka H., Demeure C., Mateo V., Rubio M., Brown E.J.,
 RA Maliszewski C., Lindberg F.P., Oldenborg A., Ullrich A.,
 RA Despease G., Sarfati M.;
 RT "Bidirectional negative regulation of human T and dendritic cells by
 RT CD47 and its cognate receptor signal-regulator protein-alpha:
 RT down-regulation of IL-12 responsiveness and inhibition of dendritic
 RT cell activation.";
 RL J. Immunol. 167:2547-2554(2001).
 CC -1- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
 CC as docking protein and induces translocation of PTPN6, PTPN11 and
 CC other binding partners from the cytosol to the plasma membrane.
 CC Supports adhesion of cerebellar neurons, neurite outgrowth and
 CC glial cell attachment. May play a key role in intracellular
 CC signaling during synaptogenesis and in synaptic function (By
 CC similarity). Involved in the negative regulation of receptor
 CC tyrosine kinase-coupled cellular responses induced by cell
 CC adhesion, growth factors or insulin. Mediates negative regulation
 CC of phagocytosis, mast cell activation and dendritic cell
 CC activation. CD47 binding prevents maturation of immature dendritic
 CC cells and inhibits cytokine production by mature dendritic cells.
 CC -1- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
 CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
 CC Binds FcR (By similarity). Binds JAK2 irrespective of its
 CC phosphorylation status and forms a stable complex. Binds SCAP1
 CC and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=P78324-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P78324-2; Sequence=VSP_007030;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=P78324-3; Sequence=VSP_007029;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
 CC Detected on myeloid cells, but not T cells. Detected at lower
 CC levels in heart, placenta, lung, testis, ovary, colon, liver,
 CC small intestine, prostate, spleen, kidney, skeletal muscle and
 CC pancreas.
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: Phosphorylated on tyrosine residues in response to
 CC stimulation with EGF, growth hormone, insulin and PDGF.
 CC Dephosphorylated by PTPN11.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC [7]
 DR EMBL: D86043; BAA12974.1; -
 DR EMBL: Y10375; CAA71403.1; -
 DR EMBL: Y11047; CAA71944.1; ALT_INIT.
 DR EMBL: AB023430; BAA87929.1; -
 DR EMBL: AC004832; AAF19260.1; -
 DR EMBL: AL034562; CAB38874.1; -
 DR EMBL: AL049634; CAB46662.1; ALT_SEQ.
 DR EMBL: AL117335; CAC12723.1; -
 DR EMBL: BC026692; AAH26692.1; -
 DR EMBL: BC033092; AAH33092.1; -
 DR EMBL: BC038510; AAH38510.1; -
 DR PIR: JCS287; JCS287.
 DR Genew: HGNC:9662; PTPNS1.
 DR MIM: 602461; -
 DR GO: GO:0005886; C:plasma membrane; TAS.
 Query Match 11.6%; Score 241.5; DB 1; Length 503;
 Best Local Similarity 25.2%; Pred. No. 4.5e-10;
 Matches 106; Conservative 64; Mismatches 163; Indels 87; Gaps 20;
 QY 8 LLLLLLFPACWAPGAGNLSQDDSPWTSDETVVAGTGVVLCQVKQKHEDSSI-----Q 61
 Db L L L L L L A A C A W S G V A G E E L Q I Q P - D K S V S V A G E S A I L H C T V -----T S L I P V G P I Q 67
 QY 62 W ---SNPAQOTLYFGEKRALDRNRIOLVTSSTPHE---LSISINVALADEGETVTCISF-- 113
 Db W R G A G P A R E L I Y - N Q E G H F R V T V S E S T K R N M D F S I S N I T P A D A G T Y C V K P K 126
 QY 114 ----TNPVETAKSLTVLGIPOKPIITGYKSLREKMDATLNCQSSGSKPA-ARLTWRKG 168
 Db G S P D T E F K S G A G T E L S V R A K P A P V V G S P A A R A T P Q H T V S F T C E S H G F S P R D I T L K W F K N 186
 QY 169 DQELHGEPTRIQEDPNKG--TTTVSSSVTFVQTRDDGASIVCSNVHESI.KGAD-RSTSQ 225
 Db G N E L S D F Q N V ---D P V G S V S V I S H S T A K V I T R E D V H S V I C E V A H V I L Q G D P L R G T A N 244
 QY 226 RIEVLYPTAMIRPDPPHPRQGLLLHCEGRG-NEVPQOYLWEKSGVPPPLKMTQESAL 284
 Db L S E T I R V P T L E V T Q Q P V R A E N Q - V N V T C Q V R K F Y P Q R L Q L T W L E N G V ---S R T E T A S T 300
 QY 285 I P F L I N K S D S G T G C T A T S N M G S Y K A Y Y I L N V -----N D P S P V P S ----- 324
 Db V ---T E N K D G T Y -----N M S W L L V N V S A H R D D V K L T C Q V E H D G Q P A V S K S H D L K 347
 QY 325 -----S S S T V H A I I G G -----I V A F T V F L L I L M I F L G H Y L R H K G T Y L T H E A K G S 370
 Db V S A H P K E G S N T A E N T G S N E R N I Y I V G V C T L L V A L L M A L Y L V R I R -----Q K A Q G S 403
 RESULT 7
 PVRL HUMAN
 ID PVRL_HUMAN STANDARD; PRT; 517 AA.
 AC Q15223; O75465; Q9HB6; Q9HBW2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
 DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
 DE (CD111 antigen).
 GN PVRL1 OR PRR1 OR HVEC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;

FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ SEQUENCE 338 AA; 37394 MW; 8FAA60AD98426B4 CRC64;
Query Match 11.7%; Score 245; DB 1; Length 338;
Best Local Similarity 27.6%; Pred. No. 1.5e-10;
Matches 86; Conservative 44; Mismatches 152; Indels 30; Gaps 13;
QY 4 PAASLLLLLLPACWAGCANLSDQSPWSTDETVAGGTWVLKCVKDHEDSSLOWS 63
Db 7 PRKQQLPVLLRLCLLPGLPVSVDFTGTDTNITVROGDTALLCFVED-RSSKVAML 65
QY 64 NPAQOTLYFGEKRALDNRIQLVTSPHELSSISINVALADGEYTCSTFTWVRTAKSL 123
Db 66 N-RSGIIFAGEDKWSLDPRVELEKRPFLYSRLRIQKVDVDEGYSYTCVQTOHPKTSQV 124
QY 124 VTVLGTPQPIITGYKSSLRKXDTATINCSGSKPAARLTWRKGGQDLHGEPTRIQEDP 183
Db 125 YLIVQPPKLSNISDTINVEGNSVTLVCMANG-RPEPVITWR-----HLPT----- 171
QY 184 NGKTFVSSSV--TFQVTRDDGASIVCSVNHSLKGDARSTSRQIEVLVYPTTAMIRPDP 241
Db 172 -GKEFGESEYELIGITREQSG-KYEKAANE-VASAD-VKQVRVTNVNPT-ITESKS 226
QY 242 PHPREQKLLHCEGRNVPQOYLWEKE-----GSVPPLQMT-QESALFFFLNKSUS 294
Db 227 NEAATGRQALLRCEASAVPTP-DFEYWRDDTRINSANGLEIKSTGSQLVMANVTTEHY 285
QY 295 GTYGCTATSNMG 306
Db 286 GNTTCVANKLG 297
RESULT 6
SHS1_HUMAN
ID SHS1_HUMAN STANDARD; PRT; 503 AA.
AC P78324; O00683; O43799; Q8N517; Q8TAL8; Q9H022; Q9UDX2; Q9UIJ6;
AC Q9Y4U9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHP8-1) (Inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (SHP-alpha-1) (SHP-alpha-2) (SHP-alpha-
DE 3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based
DE activation motifs) (Bit) (Macrophage fusion receptor) (p84).
GN PTPNS1 OR SHPS1 OR SIRP OR MYD1 OR BIT OR MFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Brain;
RX MEDLINE=97223399; PubMed=9070220;
RA Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
RA Fujioka Y., Kasuga M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes.";
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION,
RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTPN11, PTPN6 AND GRB2.
RC TISSUE=Placenta;
RX MEDLINE=97215901; PubMed=9062191;
RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ullrich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase

RT receptors.";
RL Nature 386:181-186(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
RP ARG-107; GLY-109 AND VAL-131.
RX TISSUE=Monocytes;
RC MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells.";
RL Eur. J. Immunol. 28:1-11(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
RP VAL-131.
RC TISSUE=Brain;
RX MEDLINE=20053880; PubMed=10585853;
RA Sano S.-I., Ohnishi H., Kubota M.;
RT "Gene structure of mouse BIT/SHPS-1.";
RL Biochem. J. 344:667-675(1999).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehar V.L., Lehar M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
RP GLY-109 AND VAL-131.
RX TISSUE=Brain, Kidney, and Skin;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,


```
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AF308632; AAG30281.1; -
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT SEQUENCE 515 AA; 57047 MW; BFAB00320DD3785 CRC64;
Query Match 12.0%; Score 250.5; DB 1; Length 515;
Best Local Similarity 25.9%; Pred. No. 1e-10;
Matches 116; Conservative 54; Mismatches 157; Indels 105; Gaps 25;
QY 43 GGTATLVKQVNDH-----EDSLWS-----NPAQTLVYGEKRALDRNIQL 85
DB 44 GTDVLHCSFANPLPGVKITQVTWQKATNGSKQNVATYNPANGSVLAPYR-----ERVEF 99
QY 86 VTSTPHLSISINVALADEGYTCSTPTMPRTAKSLVTLVLPQKPI--ITGYKSLR 143
DB 100 LRPSFTDGTIRLSLELEDEGVYICEFATPAGNRESQLN-LTWAKPTNWIEGTQAVLR 158
QY 144 E---KDTATL--NCQSSGSKPAALTRKQDQELHGEPTRIQE--DNGKFTTVSSVTF 196
DB 159 AKGKDDKVLVATCTSAANGKPPSVVSW---ETHLKGE-AEYQETRNPNQ-TVTVISRYRL 213
QY 197 QVTREDDGASVCSVNHSKLGADR-STSQRIEVLVYPTAMIRP-DPHPRREGQKLLHC 254
DB 214 VPSREDHRQSUACIVNH-----MDFRESLTNVQYEPVETIEFGDGNWYLRQMDVKLT 269
QY 255 EGRGNPVPQQYLWEK-EGSVPLKMTQBSALIF--PFLNKSDSGTYGCTATSNMGSKAY 311
DB 270 KADANPPATEVHTWTLNLSLPGVEAQNRTLFFRGP-INYSMAGTYICEATNPIGTRSGQ 328
QY 312 YTLNVD-----PSP-----VPSSTSTHAIIGGIVATVIFLLIMLIFLGHYLL-- 356
DB 329 VEVNITEFPYTPSPPEHGRAGQVPT-----AIGGVVSGI-----LVLVFWVGIVVAL 378
QY 357 ---RH--KGTVLTHE-----AKGSD-----APDADTATIN 382
DB 379 CRRRHTEFGDSTKHHVYNGVSKAGIQPHHPMAQNLOYPEDSDDEKXAGPLGSSVEE 438
QY 383 AEGQSGGGDDKX 394
DB 439 EEEBEGGGGERK 450
RESULT 4
PVR2_MOUSE
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ID AC PVR2_MOUSE STANDARD; PRT; 530 AA.
DT P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
GN PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene.";
RL J. Virol. 66:2807-2813(1992).
RN [2]
SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=C57BL/6; TISSUE=Brain;
RL MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus.";
RL J. Biol. Chem. 269:8431-8438(1994).
RN [3]
SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=FVB/N; TISSUE=Colon;
RL MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.R., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fallah D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.B., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2.";
RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
CC INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
```



```
DR PROSITE; P50835; IG-LIKE; 3.  
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Repeat; Alternative splicing.  
FT SIGNAL 1 20  
FT CHAIN 21 417  
FT DOMAIN 21 343  
FT TRANSMEM 344 367  
FT TRANSMEM 368 417  
FT DOMAIN 24 139  
FT DOMAIN 145 237  
FT DOMAIN 244 328  
FT DISULFID 49 123  
FT DISULFID 166 221  
FT DISULFID 266 312  
FT CARBOHYD 85 85  
FT CARBOHYD 120 120  
FT CARBOHYD 188 188  
FT CARBOHYD 237 237  
FT CARBOHYD 278 278  
FT CARBOHYD 307 307  
FT CARBOHYD 313 313  
FT VARSPLIC 386 392  
FT VARSPLIC 393 417  
FT SEQUENCE 417 AA; 45464 MW; DA4AD0F64D2F6E1F CRC64;  
Query Match 13.7%; Score 285.5; DB 1; Length 417;  
Best Local Similarity 26.2%; Pred. No. 2.4e-13;  
Matches 112; Conservative 56; Mismatches 189; Indels 71; Gaps 17;  
QY 10 LLLLLFACCAWPGCANLSQDDSQWTSDETVVA-----GGTVVLKC-QVKDHD-- 57  
DB 12 LLLTLLLSLWPP-----PQTGDIIVQATQVPGFLGDSVTLPVLOVPCMEETH 60  
QY 58 -SSLQWNPQAQ-----QTLFGEKRALRDNRIQLVLTSTPHELSISINVALADEG 106  
DB 61 VSQLTWSRHGSGSMVAFHQTGPNYSEPKLEFVAARLGTGL-RLASLRMFLGRVDEG 119  
QY 107 BYTCSIFMPVRTAKSLVTLGIPQKIITG--YKSSIREKDTATLNCSSGSPARLT 164  
DB 120 NYTCLFTVTFP-QGSRSDVIMLRVLAKPQNTAEVQVLTGKVPVVARCVSTGGPPAHIT 178  
QY 165 WRKGDQELHGPETRIQEDPN--GKTFVSSSVTFQVTRDDGASIVCSVNHSLKGADRS 222  
DB 179 WH---SDUGGNPNTSQA-PGFLSGTIVTSLWILVSSQVDGKSVTKVHESEKPKQLL 234  
QY 223 TSQRIEVLVYTTAMIRP-DPPHPREGQKLLHLHCEGRGNPVPQQYLWEKE-GSVPLKMTQ 280  
DB 235 T-VNLTVVYPPVSVISGYDNNWYLSQNEATLTCDAARSPEPTGYNWSVTMGPLPPFAVQ 293  
QY 281 ESALIFPFLNKSDSTYCTATSNMGSYKAYITLVND-PSPVPSSTYHAIIGGIYAF 339  
DB 294 QAQLLRVPDKPINTFTICNVNALGARQAELTVQKSGPPSPSGMSS-----NIIIF 347  
QY 340 IVFLLLMILFLG-----HYLIRHKGTYLTHEAKGSDDAPDADTAINT 382  
DB 348 LILGLVLLTLLIGIVFYRSCRSREFLWCHLSFSSSEHASASANGYISVSDVSREASS 407  
QY 383 ABGGQSGG 390  
DB 408 SQDPQTEG 415  
RESULT 2  
PVR_HUMAN  
ID PVR_HUMAN STANDARD; PRT; 417 AA.  
AC P15151; P15152; Q15267; Q15268;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Poliovirus receptor precursor (CD155 antigen).  
GN PVR OR PVS.
```

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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89168426; PubMed=2538245;  
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;  
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide  
RT sequence, and expression of a new member of the immunoglobulin  
RL superfamily.";  
RL Cell 56:855-865 (1989).  
RN [2]  
RP REVISIONS.  
RA Racaniello V.R.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=91006015; PubMed=2170108;  
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,  
RT Takeuchi K., Takegami T., Nomoto A.;  
RT "The poliovirus receptor protein is produced both as membrane-bound  
RT and secreted forms.";  
RL EMBO J. 9:3217-3224 (1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Kodoyanni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,  
RT Shamor M., Brower A., Olsen A.S., Smith L.M.;  
RT "Sequence analysis of a 1mb region in 19ql3.2 containing a zinc finger  
RT gene cluster.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP DOMAINS.  
RX MEDLINE=91239515; PubMed=1851992;  
RA Koike S., Ise I., Nomoto A.;  
RT "Functional domains of the poliovirus receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108 (1991).  
RN [6]  
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=93059689; PubMed=1331527;  
RA Zibert A., Wimmer E.;  
RT "N glycosylation of the virus binding domain is not essential for  
RT function of the human poliovirus receptor.";  
RL J. Virol. 66:7368-7373 (1992).  
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the  
CC cell.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and  
CC delta). Secreted (isoforms beta and gamma).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=Alpha;  
CC IsoId=P15151-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=P15151-2; Sequence=VSP_002617;  
CC Name=Gamma;  
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;  
CC Name=Delta;  
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;  
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR  
CC VIRUS BINDING AND UPTAKE.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 8.4531 Seconds

(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGPARSLLLLLLLFACWA.....AIINAEFGGSGDDKKEYFI 398

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.5	13.7	417	1	PVR CERAE
2	280	13.4	417	1	PVR CERAE
3	250.5	12.0	515	1	PVR1 PIG
4	250	12.0	530	1	PVR2 MOUSE
5	245	11.7	538	1	LAMP CHICK
6	241.5	11.6	503	1	SHS1 HUMAN
7	239	11.5	517	1	PVR1 HUMAN
8	235.5	11.3	337	1	OPCM CHICK
9	233.5	11.2	348	1	KILO RAT
10	228.5	11.0	515	1	PVR1 MOUSE
11	228.5	11.0	583	1	C166 MOUSE
12	228	10.9	538	1	PVR2 HUMAN
13	226.5	10.9	506	1	SHS1 BOVIN
14	225.5	10.8	338	1	LAMP RAT
15	225.5	10.8	583	1	C166 HUMAN
16	225	10.8	338	1	LAMP HUMAN
17	224	10.7	513	1	SHS1 MOUSE
18	221.5	10.6	702	1	CEA5 HUMAN
19	218.5	10.5	739	1	VCA1 RAT
20	217	10.4	509	1	SHS1 RAT
21	216	10.4	345	1	OPCM RAT
22	215	10.3	345	1	OPCM HUMAN
23	213	10.2	344	1	NTRI HUMAN
24	212	10.2	4391	1	PGSM HUMAN
25	211	10.1	345	1	OPCM BOVIN
26	205	9.8	344	1	NTRI MOUSE
27	204	9.8	344	1	NTRI RAT
28	202.5	9.7	353	1	CEPU CHICK
29	197.5	9.5	588	1	C166 CHICK
30	194.5	9.3	403	1	RAGE MOUSE
31	194.5	9.3	3707	1	PGSM MOUSE
32	194	9.3	547	1	ICR3 HUMAN
33	191.5	9.2	555	1	C166 CARAU

34	191	9.2	764	1	ICCR DROME
35	190.5	9.1	646	1	MU18 HUMAN
36	189.5	9.1	1447	1	DCC MOUSE
37	188	9.0	628	1	LJ HUMAN
38	187	9.0	387	1	SRB2 HUMAN
39	186	8.9	1241	1	NPHN HUMAN
40	181.5	8.7	564	1	C166 BRARE
41	181.5	8.7	1443	1	NEO1 CHICK
42	181	8.7	1377	1	NEO1 RAT
43	179	8.6	344	1	CEA6 HUMAN
44	178.5	8.6	398	1	SRB1 HUMAN
45	178.5	8.6	3375	1	UN52_CABEL

ALIGNMENTS

RESULT 1
PVR CERAE
ID PVR CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RA MEDLINE=3059651; PubMed=1331508;
RT Koike S., Ise Y., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain".
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; D12611; BAA02136.1; -;
CC EMBL; D12612; BAA02137.1; -;
CC PIR; A44194; A44194.
CC PIR; B44194; B44194.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; IG; 3.
CC SMART; SM00406; IGV; 1.

Search completed: May 27, 2004, 09:32:27
Job time : 12.5056 secs

Db 100 LPSPTDGTIRLSLELEDEGVYICFATFTGNRESQLN-LTVMAKPTNWTIEGTQAVLR 158
 QY 144 EK---DTATL--NCQSSGSKPAARLWTKGDELHGEPTRIQEDPNG--KTFVSSVTFP 196
 Db 159 AKKGQDKVLVATCATSANGKPPSVWSW---ETRLKGE-ARVPGDGTNPAPVTVISRYRL 214
 QY 197 QVTREDDGASIVCSVNHESLKGADR-STSQREVLVLTPTAMIRP-DPPHPRGQKLLHLC 254
 Db 215 VPSREAHQOQLACIVNYH-----MDRKESLTLNVQEPVETIEGDFGNWYLRQMDVKLTC 270
 QY 255 EGRGNVPQOYLWEK-EGSVPLPKMTQESALIFPF-LNKSDSGTGTCTATSNMGSYKAY 312
 Db 271 KADANPPATEYHWTTLGSLPKGVEAQNLTLPFGPINYSLAGTVICBATNPIGTRSGQV 330
 QY 313 TLNVND-----PS-----PVPSSSYTHALIGGIVAFIVELLMLLFIHGYLI--- 356
 Db 331 EVNITEFPYTPSPPEHRRAGRPVPT-----AIIQGVAGSI-----LLVLIVVGGIVVALR 380
 QY 357 --RH--KGYLT-----HEAKSGDDADPADTADTAIINAEGQSGG 390
 Db 381 RRRHTPKGDIYSTKHVYGVNGYSKAGIPIQHPPMAQNLQVDDSDDEKKA--GPLGSSSYE 438
 QY 391 DDKKE 395
 Db 439 EEEEE 443

RESULT 15
 A36319
 N;Alternate names: CEA; meconium antigen 100
 C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text change 31-Jan-2000
 C;Accession: A36319; A27773; A31037; A25845; S08106; S31737; A4476; I54224; I59098; A26
 R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Haseauer, M.; Shively,
 Mol. Cell. Biol. 10, 2738-2748, 1990
 A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
 A;Reference number: A36319; MUID:90258861; PMID:2342461
 A;Accession: A36319
 A;Molecule type: DNA
 A;Residues: 1-702 <SCH>
 A;Cross-references: GB:M17303; NID:g178676; PIDN:AA5513.1; PID:g178677
 A;Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-Thr
 R;Reauchenin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
 Mol. Cell. Biol. 7, 3221-3230, 1987
 A;Title: Isolation and characterization of full-length functional cDNA clones for human
 A;Reference number: A27773; MUID:88038876; PMID:3670312
 A;Accession: A27773
 A;Molecule type: mRNA
 A;Residues: 1-702 <BEA>
 A;Cross-references: GB:M29540; NID:g180222; PIDN:AA51967.1; PID:g180223
 R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
 Genomics 3, 59-66, 1988
 A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
 A;Reference number: A31037; MUID:89122014; PMID:3220478
 A;Accession: A31037
 A;Molecule type: mRNA
 A;Residues: 1-702 <BAR>
 A;Cross-references: GB:M29540; NID:g180222; PIDN:AA51967.1; PID:g180223
 A;Note: the authors translated the codon GTG for residue 130 as Leu
 R;Oikawa, S.; Nakazato, H.; Kosaiki, G.
 Biochem. Biophys. Res. Commun. 142, 511-518, 1987
 A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
 A;Reference number: A25845; MUID:87128144; PMID:3814146
 A;Accession: A25845
 A;Molecule type: mRNA
 A;Residues: 5-702 <OIK>
 A;Cross-references: GB:M15042; NID:g180198; PIDN:AA51963.1; PID:g180199
 submitted to the EMBL Data Library, September 1989
 A;Reference number: S08106
 A;Accession: S08106

A;Molecule type: mRNA
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 A;Cross-references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
 R;Barnett, T.
 submitted to the EMBL Data Library, September 1991
 A;Description: Genomic DNA sequence upstream of the translational start of the carcinoem
 A;Reference number: S31737
 A;Accession: S31737
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-141 <BA2>
 A;Cross-references: EMBL:X62151
 R;Khan, W.N.; Praegsmyr, L.; Teglund, S.; Israelsson, A.; Brenner, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A;Title: Identification of three new genes and estimation of the size of the carcinoembr
 A;Reference number: A4476; MUID:93052339; PMID:1427854
 A;Accession: A4476
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 35-141 <KHA>
 R;Willcocks, T.C.; Craig, I.W.
 Genomics 8, 492-500, 1990
 A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
 A;Reference number: I54224; MUID:91139118; PMID:2286372
 A;Accession: I54224
 A;Status: translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-37 <RES>
 A;Cross-references: GB:M60964; NID:g180215; PIDN:AA51964.1; PID:g180217
 R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
 A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon
 A;Reference number: I59098; MUID:87204247; PMID:3033671
 A;Accession: I59098
 A;Status: translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 331-702 <RE2>
 A;Cross-references: GB:M16234; NID:g180240; PIDN:AA51972.1; PID:g180241
 R;Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
 Biochem. Biophys. Res. Commun. 147, 212-218, 1987
 A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105
 A;Reference number: A26831; MUID:87326349; PMID:3632664
 A;Accession: A26831
 A;Molecule type: protein
 A;Residues: 35-64 <SIE>
 R;Thomas, P.; Toth, C.A.
 Biochem. Biophys. Res. Commun. 170, 391-396, 1990
 A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at t
 A;Reference number: A35490; MUID:90321257; PMID:2372297
 A;Accession: A35490
 A;Molecule type: protein
 A;Residues: 'X',140-151,'X',153,'X',155-156 <THO>
 A;Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer
 C;Comment: This heavily glycosylated membrane protein of unknown function is a widely use
 C;Comment: This protein may be processed at its C-terminus. It is anchored to the membra
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 A;Gene: GDB:CEA
 A;Cross-references: GDB:119054; OMIM:114890
 A;Map position: 19q13.2-19q13.2
 A;Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
 C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
 F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F;1-34/Domain: signal sequence #status predicted <SIG>
 F;35-678/Product: carcinoembryonic antigen #status predicted <MAT>
 F;160-217/Domain: immunoglobulin homology <IMM1>
 F;252-301/Domain: immunoglobulin homology <IMM2>
 F;338-395/Domain: immunoglobulin homology <IMM3>
 F;516-573/Domain: immunoglobulin homology <IMM4>
 F;608-657/Domain: immunoglobulin homology <IMM5>
 F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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A,Map position: 2

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Matches 112; Conservative 51; Mismatches 170; Indels 90; Gaps 20;

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DB      14 LLLCLLLSASCFCCTGVTKELKVTPQPKS-VSVAAGDSTVLNCTL-----TSLLPVGPIK 67

QY      68 QTLYFGKRAL-----RDNRIQLVTSTPH-ELISISINVALADGEYTCSTF--- 113
DB      68 WYRGVGSRLLIYFTGEHFPVTVNVSDATKRNNDFFSIRISNVTPEADAGTYVCVKPQKG 127

QY      114 -TMVTRTAKS---LVTVLGIPQKPIITGYKSSLRKQKDTATLNCSSSGSKPA-ARLTWRK 167
DB      128 PSEPTETIQSGGTEVYVLAKPSPEVSGPADRGIPDQKVNFTCKSHGSPRNITLKWFK 187

QY      168 GDQELHGEPTRIQBDPNCK--TFTVSSSVTFQVTRDDGASIVCSVNNHSLKGAADSTSQ 225
DB      188 DQQLHLETTV--NPSGKNVSNISSTVRVVLNMGMDVHSHKVICEVAHITL---DRSPLR 242

QY      226 RIE-----VLVPTAMIRDPHPREGQKLLHLCEGRGNPVPQOYLWEKEGVS---PPL 276
DB      243 GIANLSNFIKSVPTVKVTKQSPSTSNQVNLTCRAE-RFPEDILQLIWLNGVSRNDTPK 301

QY      277 KMTQESALIFPFLNKSQDGTGCTA---TSNMGSYKAYITLVN-NDPSPV----- 322
DB      302 NLT-----KNTDGTNYNTSLFLVNSAHRDQVFTQVQKHDQQAITRNHTVLG 350

QY      323 -----PSSST--YHALIGGVAFTVFLMLLMLFLGHVLIHKGTYLTHEA 367
DB      351 LAHSSDQSGMQTFPGCNATHNNWVFIGVGA---CALLVVLMAALYLLRIK-----OKKA 403

QY      368 KGS 370
DB      404 KGS 406

RESULT 14
JC4024
poliovirus receptor-related protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C:Accession: JC4024
R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr
Gene 155, 261-265, 1995
A:Title: Complementary DNA characterization and chromosomal localization of a human gene
A:Reference number: JC4024; MUID:95237621; PMID:7721102
A:Accession: JC4024
A:Molecule type: mRNA
A:Residues: 1-518 <LDP>
A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C:Genetics:
A:Gene: GDB:EVRR1
A:Cross-references: GDB:583951
A:Map position: 11q23-11q24
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: Glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F:356-379/Domain: transmembrane #status predicted <TM>
F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

QY      43 GGTWLKQCKVDHDS-----SLOWS-----NPAQOTLYFGKRALRNRQL 85
DB      44 GTDVLHCSFANLPKSVKTIQTVQKSTNGSKQNVAINPMSGVSLAPYR-----ERVEF 99

Query Match      10.6%; Score 221.5; DB 2; Length 518;
Best Local Similarity 25.9%; Pred. No. 1.5e-08;
Matches 110; Conservative 52; Mismatches 166; Indels 97; Gaps 23;

QY      86 VSTPHELSTISGNVALADGEYTCSTFTMPVTRAKSLVTVLGIPQKPI--ITGKSSLR 143

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A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-538 <RES>

A;Cross-references: GB:S79172; NID:g1042204; PID:g1042205

C;Genetics:

A;Gene: PRK2delta

C;Superfamily: poliovirus receptor; immunoglobulin homology

F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 228; DB 2; Length 538;
Best Local Similarity 24.6%; Pred. No. 5.1e-09;
Matches 93; Conservative 53; Mismatches 160; Indels 72; Gaps 15;

QY 8 LLLLLLFFACWAPGGANLSQDDSPWTSDETVVAGTVVLKQV-----52
DB 21 LLLLLL-----ETGA---QDVRVQLPEVRGQLGGTVLPCPLLPPVPLGLVSLVTWQ 71
QY 53 -----KDHE-----SSLOWNPAQOTLYF--GEKALRDNRQLQVTSIPHELSIS 96
DB 72 RPDAPANHONVAAPHKPGFSPKPGSERLSFVSQKSTGQDTEAELQDAT-----LA 126
QY 97 ISNVALADEGYTCSTFTMPRTAKSLVTVLGIPOKP--IITGVKSLREKDTATLNCS 154
DB 127 LHGLTVDEGNICEPATFPKGSVRGM-TWLRLVIAKPKNAEAKVTFSDPTVALCIS 185
QY 155 SGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSVTFQVTRDDGASIVCSVNHE 214
DB 186 KEGPPARISM-LSSLWEAKETQVSGTLAG-TVTVTSRTLVPSGRADGVTVTCRVEHE 243
QY 215 SLKGADSTSORIEVLYTPAMI-----RPDPHREGOKLLHCEGRGNPVPOQ 264
DB 244 SFE-EPALIPVTLVSRYPPVEVSGYDNNVYLGKTD-----ATLSCDVRNPSPTG 293
QY 265 YLWE-KEGSPVPLKMTQESALIFPLKNSDGTGCTATNMGSKYAYTLNNDPSPVP 323
DB 294 YDSTTSGTPTSAVAGSOLVIAVDSLENTFTVCTVNAVGNGRAEQVIFRE-TPNT 352
QY 324 SSGSYTHAIIIGVAFIV 341
DB 353 AGAGATGGIIGIIFAAII 370

RESULT 10

I39428

alcam - human

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C;Accession: I39428

R;Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, H.

J. Exp. Med. 181, 2213-2220, 1995

A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion mol

A;Reference number: I39428; MUID:95279947; PMID:7760007

A;Accession: I39428

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-583 <RES>

A;Cross-references: GB:I38608; NID:g886257; PIDN:AA859499.1; PID:g886258

Query Match 10.8%; Score 225.5; DB 2; Length 583;
Best Local Similarity 22.4%; Pred. No. 8.7e-09;
Matches 80; Conservative 70; Mismatches 148; Indels 59; Gaps 14;

QY 2 GAPAASLLLLLFFACWAPGGANLSQDDSPWTSDETVVAGTVVLKQV-----53
DB 5 GASSCLLFLCLLISATVFRPG-----LGWTVNSAY-GDTIIIPCRDLDPQNLNMF 54
QY 54 -----DHESS---LQSNPAQOTLYFGEKALRDNRQLQVTSIPHELSISINVALADEG 106
DB 55 KMRYEKPDGSPVFTAFRSSTKSVQYDDVBYKO-RLNL-----SENYSLSINARISDEK 109
QY 107 EYTCSTFTMP-VRTAKSLVTVLGIPOKPIITGVKSLREKDTATL-NCQSGSKPAARLT 164
DB 110 RFVCLMVTEDNVFEAPTVIKVFKQPSKEIVSKALFLETEQLKKLGDCISESDSPDGNIT 169

QY 165 WRKGDQELH---GEPTRI---QEDPNKGTFTVSSVTFQVTRDDGASIVCSVNHELSKG 218
DB 170 WYRNGKVLHPLLEGAVVILFEKEMDPVTQLYTWTSTLEYKTKRADIQMPFTCSVYTYGPGS 229
QY 219 ADR-STSORIEVLYTPTAMR-----PDPPHREGOKLLHCEGRGNPVPOQYLWREKGSV 273
DB 230 QKTIHSEQAVFDIYPTQVTTQVLPKNAIKEGDNITKCLONGNPPPEEFELFYLPQQP 289
QY 274 PPLKMTQESALIFPLKNSDGTGCTATNMGSKYAYTLNNDPSPVPSSSTYH 330
DB 290 EGRSSNTYTLN--DVRNATGDYKCSL-----IDKKSMTASTAITVH 330

RESULT 11

JC4776

limbic-system-associated membrane protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000

C;Accession: JC4776

R;Pimenta, A.F.; Fischer, I.; Levitt, P.

Gene 170, 189-195, 1996

A;Title: cDNA cloning and structural analysis of the human limbic-system-associated mem

A;Reference number: JC4776; MUID:96235133; PMID:8666243

A;Accession: JC4776

A:Molecule type: mRNA

A;Residues: 1-338 <PIM>

A;Cross-references: GB:U41901; NID:g1276898; PIDN:AA050569.1; PID:g1276899

A;Experimental source: brain

C;Comment: This is a neuronal surface glycoprotein distributed in cortical and subcortic

C;Genetics:

A;Gene: lamp

C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein

F;1-7/Domain: signal sequence #status predicted <SIG>

F;333-338/Region: hydrophobic

F;40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status pred

F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted

F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 10.8%; Score 225; DB 2; Length 338;

Best Local Similarity 25.4%; Pred. No. 4.7e-09;

Matches 91; Conservative 55; Mismatches 172; Indels 40; Gaps 15;

QY 4 PAASLLLLLFFACWAPGGANLSQDDSPWTSDETVVAGTVVLKQVQKHEDSSIQWS 63

DB 7 PDRKQLPLVLLRLCLLPTGLPVRSVDFNRGTDNITVRQDGTAILRCVLED-KNSKVAVL 65

QY 64 NPAQOTLYFGEKALRDNRQLQVTSIPHELSISINVALADEGYTCSTFTMPVRTAKSL 123

DB 66 N-RSGIIFAGHDKMSLDPRVELEKRSLSYLRQKVDVDEGYSYCSVQTHPEPKTSQV 124

QY 124 VTVLGIPOKPIITGVKSLREKDTATLNCSGSKPAARLTWRKGDQELHGEPTRIQEDP 183

DB 125 YLIVQVPPKLSNSTDVTVNMGSNVILCVANG-RPEPVITWR-----HLTPT----- 171

QY 184 NGKTFVSSSV--TFQVTRDDGASIVCSVNHELSKGADSTSORIEVLYTPTAMIRPDP 241

DB 172 -GREFEEEEEYLEILGITREQSG-KVECKAANE-VSSAD-VKQKVTVNVPPT-ITESKS 226

QY 242 PHREGOKLLHCEGRGNPVPOQYLWKE-----GSVPLKMTQ-ESALIFPLNKS 294

DB 227 NEATTGQASLKCEASAVPAP-DFEYWRDTRNNSANGLEIKTEGSSSLTVTNVTEHY 285

QY 295 GTYGTCTATNMGSKYAYTLNNDPSPVPSSSTYTHAIIIGI-VAFIVFLLIIMLIEL 351

DB 286 GNYTCVAANKLG-----VTNASLVLRPGRSVRGINGSISLAVPLWLLASLLCL 334

RESULT 12

JC5288

SHP substrate-1 protein, 509 - mouse

C;Species: Mus musculus (house mouse)

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Db      47  GGTVELPCHLLPPTTERRVSVQVWRLDGTWAAFHPS-----FGVDFPNSQFSKORLSFV 101
QY      87  TSSTP-----HELISISINVALADEGEYTCSTFTMPVRTAKSLVTLVGLPQKP--IIITGV 138
Db      102  RARPETNADLRDATLAFRGLRVEDEGNYCEFAFPNGFRG-VTWLRVIAQEPENHAEQA 160
QY      139  KSLIREKDTATLNCQSSGSKPAARLWRKGDQELHGEPTRIQEDP-NGKTFVTSSSVTFQ 197
Db      161  EVTIGSQSVAVARCVSTGGRPPARIW---ISLSGGEAKDTQEPGAGVTIISYSLV 217
QY      198  VTRDDDCASIVCSVNHESLKGADRSTSQRIEVLVYTPAMIRPPHPREG-----Q 248
Db      218  PVGRADGVKVTCTVERHESPEE-----PILLPVTLVSRVPPEVSISGYDDNWLGRS 268
QY      249  KLLHLEGGRNPVPOQYLWE-KGSSVPLKQWQTESALIPFLNKSQSGTGTCTATSNMGS 307
Db      269  EAILTCVRSNPFPTDYDWTSGVFPASAVAGSQSLVHSVDRMWNMTTFCITATNAVT 328
QY      308  YKAYVTLNVNDPSPVPSSTYHAIIGVIAFTVFLILLMLIFLGHYLIIRHKGYTLTHEA 367
Db      329  GRAEQVILVD---TPQASRDVGLVWAGVGLLVLLLAGGLALILLRGRRRRSPGG 385
QY      368  KGSDDAPDADTAIINAEQSGSGDKKEYF 397
Db      386  GGND-----GDRGSYDPKTVQV 402

RESULT 7
JC5519
50K glycoprotein precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
C:Accession: JC5519
R:Hancock, K.A.; Gooley, A.A.; Jeffrey, P.I.
Mol. Brain Res. 44, 273-285, 1997
A:Title: AvGp50, a predominantly axonally expressed glycoprotein, is a member of the IgL
A:Reference number: JC5519; MUID:97225899; PMID:9073169
A:Accession: JC5519
A:Molecule type: mRNA
A:Residues: 1-338 <HAN>
A:Experimental source: brain
C:Comment: This protein belongs to the IgLON's subfamily of cell adhesion molecules.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-338/Product: 50K glycoprotein #status predicted <IM1>
F:146-199/Domain: immunoglobulin homology <IM2>
F:232-292/Domain: immunoglobulin homology <IM3>
F:40,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 11.6%; Score 243; DB 2; Length 338;
Best Local Similarity 27.6%; Pred. No. 2,3e-10;
Matches 86; Conservative 44; Mismatches 152; Indels 30; Gaps 13;

QY      4  PAASLLILLPACCAWPGGANLSQDQSPWTSDBTVVAGTVVLKQVQKHEDSSLOWS 63
Db      7  PDRKQLPLVLLRLCLLPTGLPVRSDFTGRDNTVTRQDGTAILRCFVED-RSSKVAWL 65
QY      64  NPAQOTLYPGEKRALRDNRILQVLTSTPHELISISINVALADEGEYTCSTFTMPVETAKSL 123
Db      66  N-RSGIIFAGEDKWSLDPRVELEKRSPLSEYSRIQKVDVYDEGSYTCVSQTOHHPTKSOV 124
QY      124  VTVLGLPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLWRKGDQELHGEPTRIQEDP 183
Db      125  YLIVQVPPKINSISSDITVNESNVTLCWANG-REPVEITWR-----HLTFT----- 171
QY      184  NGKTFVTSSSV--TFQVTRDDGCASIVCSVNHESLKGADRSTSQRIEVLVYTPAMIRPP 241
Db      172  -GKEFGSEBEYLEILGITREQSG-KYECKAANE-VASAD-VKQVRVTVNVPPT-ITESKS 226
QY      242  PHRREGQKLLHCEGRGNVPVQOYLWEKE-----GSVPLKMT-QESALIPFLNKSQS 294

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Db      227  NEATGROALLPCEASAVPTP-DFEWYRDDTRINSANGLEIKSTGSQSLIMVAVTEEHY 285
QY      295  GTYGTATSNMG 306
Db      285  GNYTCVAANKLG 297

RESULT 8
JC5287
SHP substrate-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC5287
R:Yamamoto, T.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A:Reference number: JC5287; MUID:97223399; PMID:9070220
A:Contents: Brain
A:Accession: JC5287
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-503 <YAM>
A:Cross-references: DDBJ:D86043; NID:gl864010; PIDN:BAA12974.1; PID:gl864011
C:Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C:Genetics:
A:Gene: shps-1
A:Map position: 20p13

Query Match 11.6%; Score 241.5; DB 2; Length 503;
Best Local Similarity 25.2%; Pred. No. 4,8e-10;
Matches 106; Conservative 64; Mismatches 163; Indels 87; Gaps 20;

QY      8  LLLLLLACCAWPGGANLSQDQSPWTSDBTVVAGTVVLKQVQKHEDSSSL-----Q 61
Db      14  LLCLLLAASCWAGVAGEELQVIQP-DKSVSVAAGESAILHCTV-----TSLIPVGP 67
QY      62  W---SNPAQOTLYPGEKRALRDNRILQVLTSTPHE---LSISINVALADEGEYTCSTF-- 113
Db      68  WFRGAGPARELIY-NQKEGHFRVTVTSESTKKNMDFISISNITPADAGTYCVKFRK 126
QY      124  ---TMPVRTAKSLVTLVGLPQKPIITGYKSSLRKDTATLNCQSSGSKPA-ARLTWRKG 168
Db      127  GSPDTEFKSAGTSLVRAKSPVSVGPAARATPQHTVTSFTCESHGFSRDIITLWFKN 186
QY      169  DQELHGEPTRIQEDPQK--TFTVSSSVTFQVTRDDGCASIVCSVNHESLKGAD-RSTSQ 225
Db      187  GNELSDFTQNV--DPVGESVSYSIHTAKVLTREDVHVSQVCEVAHVTLQGDPLRGATN 244
QY      226  RIEVLVYTPAMIRPPHPREGQKLLHCEGRG-NPVPQOYLWEKGSVPPLKMTQESAL 284
Db      245  LSETIRVPPTLVTQVPRANQ--VNTCQVRKFPQRLQTLWLENGV---SRTEAST 300
QY      285  IFPELNKSDSGTGTCTATSNMGSYKAYITLVN-----NDPSPVPS----- 324
Db      301  V-----TENKDTY-----NMSWLLNVNSAHRDDVKLTQCVHEDGQPAVSKSHDLK 347
QY      325  -----SSSTYHAIIGG-----IVAFIVFLLIMLIFLGHYLIIRHKGYTLTHEAKGS 370
Db      348  VSAHPKEQSGNTAAENTGSNERNIYVGVVCTLLVALLMAALYLVRIR-----QKKAQGS 403

RESULT 9
I68093
PRR2 delta - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I68093
R:Berberie, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I68093

```

A:Cross-references: EMBL:X64116; NID:g35809; PIDN:CRA45478.1; PID:g825708
A:Note: 67-Ala was also found
A:Note: the gamma form has 331-Gly and lacks residues 332-384
R:Wendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expression
A:Reference number: A90910; MUID:89168426; PMID:2538245
A:Accession: A31496
A:Molecule type: mRNA
A:Residues: 1-66, 'A', 68-417 <MEN>
A:Cross-references: GB:M29535
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F:21-343/Domain: extracellular #status predicted <EXT>
F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F:42-125/Domain: immunoglobulin homology <IMM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.5%; Score 281; DB 1; Length 417;
Best Local Similarity 28.0%; Pred. No. 4.8e-13;
Matches 108; Conservative 50; Mismatches 158; Indels 70; Gaps 17;

QY 5 AASILLILLFACWAPGGANLSQDDSQPWTSETVA-----GGTVLKC--QVKD 54
DB 7 AAWPLLVALLVLSWPP-----PGTGDVVVQAPQVPGFLGDSVTLFCYLOVNP 55

QY 55 HE---DSLSQNSPAQTLVFEKRAL-----RDNIQLVSTPHELSISIN 99
DB 56 MEVTHVSQLTWTR-----HGSGGSAVHFQTOGSPYSSESKLLEFVAA---RLGAELRN 105

QY 100 VAL-----ADEGEYTCSTFTMPVRTAKSLVTLVGLPQKPIIFG--YKSLREKDTATL 150
DB 106 ASLRFMLGRVDEGNYCTLFTFP--QGSRSVDIWLRLAKPONTAEVQKVLQTPVPMA 164

QY 151 NCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPN--GKTFVSSSVTFQVTRDDGASIV 208
DB 165 RCVSTGGRPPAQITWH---SDLGMPNTSQV--PGFLSGVTVTLSLWILVSSQVDGKNVT 220

QY 209 CSVNHESLKGADRTSQRIEVLYPTAMIRDPDPHPREGQ--KILLHCEGRGNPVPQOYLW 267
DB 221 CKVHESEFEKQLLT--VNLITYYPPEVVISGYDNNWYLGNEATLTCDARSNPETGVNW 279

QY 268 EKE--GSPVPLPKMTQESALIFPFLNKSQSGTGCATSNMGSYKAYITLVNNDPSPVSSS 326
DB 280 STTWGPLPPFAVAGQAQLLRVDPKPIINTLTCNVNLTALGARQAELTVQVKEGPPSEHS 339

QY 327 STYHAIIGGIVAFIVFLLIMLIFLG 352
DB 340 MSRNAIL-----FLVLGILVFLILLG 360

RESULT 5
A53437
poliovirus receptor mPVR - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8436, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with p

A:Reference number: A53437; MUID:94179228; PMID:8132569

A:Accession: A53437

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-530 <AOX>

A:Cross-references: GB:D56107; NID:g475017; PIDN:BAA05103.1; PID:g825507

A:Experimental source: C57/BL6, brain

A:Note: sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 12.0%; Score 250; DB 2; Length 530;

Best Local Similarity 25.7%; Pred. No. 1.2e-10;

Matches 86; Conservative 49; Mismatches 145; Indels 54; Gaps 13;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 11.5056 Seconds

(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPAAALLLLLLLFACCA.....AIINAEGGSGGDKKEYFI 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.5	13.7	417	2 A44194	poliovirus recepto
2	284	13.6	392	2 B44194	poliovirus recepto
3	281	13.5	392	1 RWHUPD	poliovirus recepto
4	281	13.5	417	1 RWHUPA	poliovirus recepto
5	250	12.0	530	2 A53437	poliovirus recepto
6	248.5	11.9	467	1 HLMSP3	poliovirus recepto
7	243	11.6	338	2 JC5519	50K glycoprotein p
8	241.5	11.6	503	2 JC5287	SHP substrate-1 pr
9	228	10.9	538	2 I68093	PRR2 delta - human
10	225.5	10.8	583	2 T39428	alcam - human
11	225	10.8	338	2 JC4776	limbic-system-asso
12	224	10.7	509	2 JC5288	SHP substrate-1 pr
13	224	10.7	513	2 JC5289	SHP substrate-1 pr
14	221.5	10.6	518	2 JC4024	poliovirus recepto
15	221.5	10.6	702	2 A36319	carcinoembryonic a
16	218.5	10.5	739	2 JS0675	vascular cell adhe
17	218	10.5	5175	2 T20992	hypothetical prote
18	218	10.5	5198	2 T43290	hemiscatin precurs
19	216.5	10.4	338	2 JC1238	opioid-binding pro
20	216	10.4	345	2 JC1239	opioid-binding pro
21	216	10.4	478	2 JS3960	PRR2 alpha - human
22	215	10.3	345	2 JC4025	opioid-binding cel
23	211	10.1	345	2 S03199	opioid-binding pro
24	210.5	10.1	1612	2 T30805	duttl protein - mo
25	209	10.0	4391	2 A38096	perlecan precursor
26	204.5	9.8	1651	2 T4160	transmembrane rece
27	204	9.8	344	2 JS6551	neurotrophin - rat
28	203.5	9.8	7962	2 I38346	elastic titin - hu
29	197.5	9.5	588	2 JH0506	adhesion molecule

30 197.5 9.5 588 2 A45254 surface glycoprote
31 195 9.3 402 2 T09062 probable advanced
32 194.5 9.3 3707 2 S18252 heparan sulfate pr
33 194 9.3 547 1 S28904 intercellular adhe
34 191.5 9.2 1427 2 I51669 tumor suppressor -
35 191 9.2 764 2 A49448 irregular chiasm C
36 190.5 9.1 646 2 I38049 cell surface glyco
37 189 9.1 407 2 T08732 hypothetical prote
38 188 9.0 628 2 I38000 Lutheran blood gro
39 187.5 9.0 523 2 I50478 neurulin - goldfis
40 187.5 9.0 4162 2 T42633 connectin/titin -
41 186 8.9 1241 2 T37190 nephrin - human
42 184 8.8 588 2 I37202 B-CAM protein - hu
43 183.5 8.8 584 2 I50419 s-glycerin precurs
44 182.5 8.7 416 2 A54017 colon carcinoma-as
45 182.5 8.7 587 2 JH0464 DM-GRASP precursor

ALIGNMENTS

RESULT 1

A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: A44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no put
A;Reference number: A44194; MUID:93059631; PMID:1331508
A;Accession: A44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 13.7%; Score 285.5; DB 2; Length 417;
Best Local Similarity 26.2%; Pred. No. 2.3e-13;
Matches 112; Conservative 56; Mismatches 189; Indels 71; Gaps 17;
Qy 10 LLLLLFACCAWAGGANSQDQSPWTSDETVVA-----GGTVLKC--QVKDHE-- 57
Db 12 LLLTLLLELWPP-----PGTGDIIVQAPTQVPGFLGDSVTLPCYLQVGMEEH 60
Qy 58 -SSIQMSNPAQ-----QTLYFGEKRALDRNRIOLVTSPTHELSISISNVALADEG 106
Db 61 VSQLTWSRHGSGSMVPHOTQGNVSEPRLEFVAARLGTTEL-RDASLRFGLRVEDEG 119
Qy 107 EYTCSTFTMPVRTAKSLVTVLGIPOKEIITG--YKSSLREKDTATLNCSSGSKPAARLT 164
Db 120 NYTCLFTTTP-QGSRSDVDIWLRLVLAKEQNTAEVKQVLTGKVPVAVCVSTGGRPAAHT 178
Qy 165 WRKGDQBLHGEPRIQEDPN--GKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRS 222
Db 179 WH---SDLGGMPTNSQA-PGFLSGTVTVTSLIWLVPSSQVDGKSVTKVEHSEPKQLL 234
Qy 223 TSQRIEVLVYFTAMIRP-DPPHPREGOKLLHCEGRGNVPVQQYLWEKE-GSVPLPKMTQ 280
Db 235 T-VNLTVVYPEVVISGYDNNVYLSQNEAVITCDARNPEPTGNWMTTGWLPFFFAVAQ 293
Qy 281 ESALIFPFLNKSQGTGCTATSNMGSYKAYTYTLNVND-PSPVSSSSSTYHAITGIVAF 339
Db 294 GAQLLIPVDKPIINTFTICNVTNALGARQALITVQVKEGPPSEPSGWS-----NIIF 347
Qy 340 IVFLLLLIMLIFLG-----HYLRHKGTLYLTHEAKGSDDDAPDADTAIIN 382
Db 348 LILGIVILLTLLGIGVYFYRSCRSREFLWCHLSPSSEEHASANGYISYSDVSREASS 407
Qy 333 AEGGQSGG 390

US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules D

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QY 122 STPHLSISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKEDT 181
Db 91 ASWHELSISVSDSLSDGEGYTCSLFTMPVKTSKAYLTVLGVEPEKQISGFSPVNEGDL 150
QY 182 ATLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGAS 241
Db 151 MQLTCKTSGSKPAADIRFWKNDKEIKDVYKLEEDANRKTFTVSSTLDFRVDSDGAV 210
QY 242 VCSVNHESLKADRSQRIEVLVYTPMTAMIRPDPHPHREGOKLLHCEGEGNVPQOYLW 301
Db 211 ICRVDHESLNATQVAMQVLEIHYTPSVKIPSTPPFQEGQPLITCESKGLPLBEVLW 270
QY 302 EKEGSV---PPLKMTQESALIFPFLNKSQSGTGTATSNMGSYKAYYTLNVNDP----- 352
Db 271 TKDGELPDPDRMVVSGRELNIPLNKTNGTYRCEATNIGQSSARYVLIVHDPNTLL 330
QY 353 PSPV-----PSSSTY-----HAIIGVIAFIVFLL 378
Db 331 PTTIIPSLTATVTTVAITTSPTTSATTSIRDPNALAGQDPDHALIGIVAVVFT 390
QY 379 LIMLIFLGHYLRHKGYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 432
Db 391 LCSIFLLGRYLARKGYLTNEAKGADPADPADTAIINAEQSGVNABEKKEYFI 444

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RESULT 12
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/866,028
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

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Query Match 32.0%; Score 723.5; DB 4; Length 440;
Best Local Similarity 36.2%; Pred. No. 7e-57;
Matches 168; Conservative 74; Mismatches 145; Indels 77; Gaps 10;

QY 3 APAASLLILLFACCWAPGGANLSODGYWQEOLEGLTAPLDEAISSTVSSPDMLAS 62
Db 20 APGLRLLLLFSAALIPG-----DG-----QNL----- 45
QY 63 QDSQPWTSDETAVAGTIVLKQVKDHEDSSLOWNPAQOTLYFGKRALRDNRIQLVTS 122
Db 46 -----FTKDVTVIEGEVATISCVQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLNLF 100
QY 123 TPHELSISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKEDTA 182

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Db 101 SSSELKVLNTVNSISDEGRYFCQLYTDPPEBSYTTITVLVPPRNLMDIQKTAVEGEI 160
QY 183 TLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGASIV 242
Db 161 EYNCTAMASKPATIRFWKNTLKGK-SEVEWSD--MYTITSQMLKVKHEDDGVPI 217
QY 243 CSVNHESLKADRSQRIEVLVYTPMTAMIRPDP-----HPREGOKLLHCEGEGNVPQOY 299
Db 218 CQVEHPAVTG-NLQTVLEVOYKQVHIQMTYPLQGLTREGDALELTCEAIGKPOVMV 276
QY 300 LWEK-EGSVPLKMTQESALIFPFLNKSQSGTGTATSNMGSYKAYYTLNVNDP-----P 355
Db 277 TWVRVDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASINVGKASDYMLYVDPPTIP 336
QY 356 VPSSSTY-----HAIIGVIAFIVFLLLMILFIHGY 388
Db 337 PPTITTTTTTTTTTTITITDSRAGEBSIRAVDHAVIGGVAVVVFAMCLLIILGRY 396
QY 389 LIHKGYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 432
Db 397 FARHKGTYFTHAKGADDAADADTAIINAEQSGQNSEKKEYFI 440

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RESULT 13
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

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Query Match 31.9%; Score 722; DB 4; Length 442;
Best Local Similarity 36.4%; Pred. No. 9.6e-57;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

QY 4 PAASLLILLF-ACCWAPGGANLSODGYWQEOLEGLTAPLDEAISSTVSSPDMLAS 62
Db 22 PGLRLRLLLLFSAALIPG-----DG-----QNL----- 47
QY 63 QDSQPWTSDETAVAGTIVLKQVKDHEDSSLOWNPAQOTLYFGKRALRDNRIQLVTS 122
Db 48 -----FTKDVTVIEGEVATISCVQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLNLF 102
QY 123 TPHELSISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKEDTA 182
Db 103 SSSELKVLNTVNSISDEGRYFCQLYTDPPEBSYTTITVLVPPRNLMDIQKTAVEGEI 162
QY 183 TLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGASIV 242
Db 163 EYNCTAMASKPATIRFWKNTLKGK-SEVEWSD--MYTITSQMLKVKHEDDGVPI 219
QY 243 CSVNHESLKADRSQRIEVLVYTPMTAMIRPDP-----HPREGOKLLHCEGEGNVPQOY 299
Db 220 CQVEHPAVTG-NLQTVLEVOYKQVHIQMTYPLQGLTREGDALELTCEAIGKPOVMV 278
QY 300 LWEK-EGSVPLKMTQESALIFPFLNKSQSGTGTATSNMGSYKAYYTLNVNDP-----P 355
Db 279 TWVRVDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASINVGKASDYMLYVDPPTIP 338

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302	QY	EXEGSV---	PLIKMTQESALIFPLNKS	DSGTCTATSNM	SGYKAYTYLNVND-----	352
248	Db	TKDGELPDP	PMVVSGRELNLFLNK	TDCNGTYRCEATN	IGQSSAEYVLIVHDEVTELL	307
353	QY	PSPV-----	PSSTSY-----	HAITGGIVAF	TVFL	378
308	Db	PTIIPSLT	TATVTTTVAITTSPT	TSSIRPNALAGQ	PDHALIGIVAVVVFVT	367
379	QY	LIMLFLG	HYLIRHKGTYLTHEA	KGSDDAPADP	ATAINAEQSGGDDKKEYFI	432
368	Db	IGSIFL	GLRYLARHKGTYLTHEA	KGADAPADP	ATAINAEQSQVNAEKKEYFI	421

RESULT 10
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match	44.9%;	Score	1017.5;	DB	2;	Length	444;
Best Local Similarity	48.6%;	Pred. No.	2e-83;				
Matches	201;	Conservative	70;	Mismatches	100;	Indels	43;
Gaps	4;						
QY	62	SODSQPWTSDFTVWAGGTVVLKCVKQVHEDSSLOWNSPAQOTLTFGEKRALDRNRIQLVT	121				
Db	31	SOQGFPLQNTVVEGGTALLTCRDQNDNTSLQNSPAQOTLYPDDKKALDRNRIELVR	90				
QY	122	STPHSELISISNVALADEGEYTCSTFTMPRTAKSLTVVLGIPQKPIITGVKSSUREKDT	181				
		:::	:::	:::	:::	:::	:::
Db	91	ASWHSELISVSDVSLSDGEQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFSPPWMEGDL	150				
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QY	182	ATINQSSGSKPAARLTVWRKGDQELHGEPTRIQEDPNKGKTFVTSSSVTFQVTTREDDGASI	241				
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[illegible]

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	Query Match	44.9%	Score 1017.5	DB 3	Length 444
	Best Local Similarity	48.6%	Pred. No. 2e-83		
	Matches 201	Conservative	70	Mismatches 100	Indels 43
					Gaps 4
Qy	62	QSDSQPMTSDATVWAGGTVLWLCVKQKHEDSSLOWNSPAQOTLYFGKRALRDNRILVLT	121		
ph	31	SGOGFPIITONTVWVGSGTALITCTVDNDNTSLWSNPAAOTLYFDKKAALRDNRIELVR	90		

RESULT 8

US-08-659-984A-1
 ; Sequence 1, Application US/08659984A
 ; Patent No. 5942400
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Jacobson-Croak, Kirsten L.
 ; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 ; TITLE OF INVENTION: Inhibition
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/659,984A
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,152
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002810US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-659-984A-1

Query Match 44.9%; Score 1017.5; DB 2; Length 421;
 Best Local Similarity 48.6%; Pred. No. 1.9e-83;
 Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;
 QY 62 SQDSQPWTSDETVVAGTVVVKCOVKDHEDSSLOWNSPAQOTLYFGKRALRDNRIQLVT 121
 DB 8 SQGQFPILTQNTVVVEGGTALTCTCRVDQNDNTSLQNSNPAQOTLYFDDKALRDNRIELVR 67
 QY 122 STPHLSISISNVALADEGYTCSTFTMPVTRAKSLVTLVGIPOKPIITGVKSSLRKDT 181
 DB 68 ASWHLSISVSDVLSDEGQVTCSTFTMPVTRAKSLVTLVGIPOKPIITGVKSSLRKDT 127
 QY 182 ATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASI 241
 DB 128 MQLTCKTSGSKPAADIRFKNDEIKDVKYLKEEDANKRTFTVSTLDFRVDSDDGAV 187
 QY 242 VCSNVHESLKGADRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPVQYLW 301
 DB 188 ICRVDHESLNATPQVAMQVLEIHYTPSKAYLTVLGVPEKPOISGFSFPMEGDL 247
 QY 302 EKEGVS---PPLKMTQESALIPFFLNKSDSGPYGTCATSNMGSKYAYTYLNNV----- 352
 DB 248 TKDGGELPDRMVMVSGRELNLFLNKTNDNGTYRCEATNTICQSSAEVYLIHVDPNTLL 307
 QY 353 PEPV-----PSSSY-----HAIIGGVAIVFLL 378

DB 308 PTTIIPSLTATVTTTVAITTSPTTSATTSIRDPNALAGQDPHALIGGIVAVVFTV 367
 QY 379 LIMLIFLGHLYLRHKGYTLTHEAKGSDPADADTAITAINAEGQSGGDDKXYYFI 432
 DB 368 LCSIFLLGRYLARHKGTVLTNEAKGAEDAPADTAITAINAEGSQVNAEKKEYFI 421
 RESULT 9
 US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Query Match 44.9%; Score 1017.5; DB 3; Length 421;
 Best Local Similarity 48.6%; Pred. No. 1.9e-83;
 Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;
 QY 62 SQDSQPWTSDETVVAGTVVVKCOVKDHEDSSLOWNSPAQOTLYFGKRALRDNRIQLVT 121
 DB 8 SQGQFPILTQNTVVVEGGTALTCTCRVDQNDNTSLQNSNPAQOTLYFDDKALRDNRIELVR 67
 QY 122 STPHLSISISNVALADEGYTCSTFTMPVTRAKSLVTLVGIPOKPIITGVKSSLRKDT 181
 DB 68 ASWHLSISVSDVLSDEGQVTCSTFTMPVTRAKSLVTLVGIPOKPIITGVKSSLRKDT 127
 QY 132 ATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASI 241
 DB 128 MQLTCKTSGSKPAADIRFKNDEIKDVKYLKEEDANKRTFTVSTLDFRVDSDDGAV 187
 QY 242 VCSNVHESLKGADRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPVQYLW 301
 DB 188 ICRVDHESLNATPQVAMQVLEIHYTPSKAYLTVLGVPEKPOISGFSFPMEGDL 247

Db 30 ---DSQWTSDETVAGGVVLKCOVKHEDSSLOWNSPAQOTLYFGEKRALRDNRIQLV 86
Qy 121 TSTPHLSISINVALADEGEVTCISFTMPVRTAKSLVTLVIGIPQKPIITGYKSSLRKED 180
Db 87 SSTPHLSISINVALADEGEVTCISFTMPVRTAKSLVTLVIGIPQKPIITGYKSSLRKE 146
Qy 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTTFTVSSSVTFQVTRDDGAS 206
Qy 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 300
Db 207 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYV 266
Qy 301 WEKESGVPPLKMTQESALIPFPLNKSQSGTGTATSNMGSKYKAYTTLNNDPSPVPSSS 360
Db 267 WYKESGSEPLKMTQESALIPFPLNKSQSGTGTATSNMGSKYKAYTTLNNDPSPVPSSS 326
Qy 361 STVHAIIGGVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPDADTAIINAE 420
Db 327 STVHAIIGGVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPDADTAIINAE 386
Qy 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 7

US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 947
; LENGTH: 227
; TYPE: PFT
; ORGANISM: Homo sapiens
US-09-205-258-947
Query Match 52.5%; Score 1189; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4e-99;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 126 ELSISINVALADEGEVTCISFTMPVRTAKSLVTLVIGIPQKPIITGYKSSLRKDTATLN 185
Db 1 ELSISINVALADEGEVTCISFTMPVRTAKSLVTLVIGIPQKPIITGYKSSLRKDTATLN 60
Qy 186 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTTFTVSSSVTFQVTRDDGASIVCSV 245
Db 61 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTTFTVSSSVTFQVTRDDGASIVCSV 120
Qy 246 NHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYLWEKEG 305
Db 121 NHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYLWEKEG 180
Qy 306 SVPLKMTQESALIPFPLNKSQSGTGTATSNMGSKYKAYTTLNND 352
Db 181 SVPLKMTQESALIPFPLNKSQSGTGTATSNMGSKYKAYTTLNND 227

RESULT 5
US-09-778-187b-8.rai
; Sequence 84, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902.775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84

; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84
Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLLLLFFACCCWAPGGANLSQDGYWQEQDLELGTALPLDEALISTVWSSPDML 60
Db 1 MGAPAAASLLLLLLLLLFFACCCWAPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVAGGTWVWKCOVKDHEDSSLOWNSPAQQTLYFGEKRALRDNRIQLV 120
Db 30 ---DSQFWTSDETVAGGTWVWKCOVKDHEDSSLOWNSPAQQTLYFGEKRALRDNRIQLV 86
QY 121 TSTPHELSSISNVALADEGEVTCSTFTMPVRTAKSLVTLVGLIPQKPIITGYKSSLEKRD 180
Db 87 TSTPHELSSISNVALADEGEVTCSTFTMPVRTAKSLVTLVGLIPQKPIITGYKSSLEKRD 146
QY 181 TATLNCSSGSKPAARLTWRKGOELHGPETRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKGOELHGPETRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHPRGQKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHPRGQKLLHCEGRGNPVPQOYL 266
QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTTLNVNDSPPVSSS 360
Db 267 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTTLNVNDSPPVSSS 326
QY 361 STTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTALINAE 420
Db 327 STTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTALINAE 386
QY 421 QSGGDDKKKEYFI 432
Db 387 QSGGDDKKKEYFI 398
RESULT 6
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4
Query Match 86.4%; Score 1955; DB 4; Length 398;
Best Local Similarity 87.5%; Pred. No. 3.8e-168;
Matches 378; Conservative 11; Mismatches 9; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLLLLFFACCCWAPGGANLSQDGYWQEQDLELGTALPLDEALISTVWSSPDML 60
Db 1 MGAPAAASPVPLLLLLLACSWAPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVAGGTWVWKCOVKDHEDSSLOWNSPAQQTLYFGEKRALRDNRIQLV 120

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Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPASLHLLHLLFACCCWAPGANLSQDGYOEQDLGLTAPLDEAISTWSSPDML 60
Db 1 MGAPASLHLLHLLFACCCWAPGANLSQD-----29
QY 61 ASODSQWTSDETVAGGTVVLKQVKDHEDSSLOWSNPAQOQTLFYFGEKRALDRNRIQLV 120
Db 30 ---DSQWTSDETVAGGTVVLKQVKDHEDSSLOWSNPAQOQTLFYFGEKRALDRNRIQLV 86
QY 121 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDOELHGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 240
Db 147 TATLNCSSGSKPAARLTWRKQDOELHGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 360
Db 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 326
QY 361 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDPADADTAINAEGG 420
Db 327 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDPADADTAINAEGG 386
QY 421 QSGGDDKKKEYFI 432
Db 387 QSGGDDKKKEYFI 398

```

RESULT 4

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US-09-905-125A-84
; Sequence 84, Application US/0905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/05125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

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Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPASLHLLHLLFACCCWAPGANLSQDGYOEQDLGLTAPLDEAISTWSSPDML 60
Db 1 MGAPASLHLLHLLFACCCWAPGANLSQD-----29
QY 61 ASODSQWTSDETVAGGTVVLKQVKDHEDSSLOWSNPAQOQTLFYFGEKRALDRNRIQLV 120
Db 30 ---DSQWTSDETVAGGTVVLKQVKDHEDSSLOWSNPAQOQTLFYFGEKRALDRNRIQLV 86
QY 121 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDOELHGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 240
Db 147 TATLNCSSGSKPAARLTWRKQDOELHGEYTCISFTMPVPTAKSLVTVLGIPOKPIITGYKSSLRKD 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 360
Db 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 326
QY 361 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDPADADTAINAEGG 420
Db 327 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDPADADTAINAEGG 386
QY 421 QSGGDDKKKEYFI 432
Db 387 QSGGDDKKKEYFI 398

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US-09-905-125A-84

Query Match 90.9%; Score 2059; DB 4; Length 398;

Best Local Similarity 92.1%; Pred. No. 1.6e-177;

Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYLTHKAGSDDDADDTAIIAEGG 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYLTHKAGSDDDADDTAIIAEGG 420
QY 421 QSGGDDKKEYFI 432
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 QSGGDDKKEYFI 432

RESULT 2

US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778.510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYQWQEDLELGTIAPLDEAISTVWSSPDM 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MGAPAAALLLLLLFACCAWPGGANLSQD----- 29
QY 51 ASQDSQPMSTDETAVAGTIVLKCQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
30 ---DSQPMSTDETAVAGTIVLKCQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 86
QY 121 TSTPHEISISNVALADEGYTCSIFTMPVRTAKSLVTLGIPKPIITGYKSSLEK 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
87 TSTPHEISISNVALADEGYTCSIFTMPVRTAKSLVTLGIPKPIITGYKSSLEK 146
QY 181 TATLNCQSSGKPAARLTWRKGDQELHGEPTRIQBDPNKGTFTVSSSVTFQVTRDDGAS 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
147 TATLNCQSSGKPAARLTWRKGDQELHGEPTRIQBDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRTSQRLEVLTPMTIRPDPPHREGQKLLHCEGRNVPVQOYL 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 IVCSVNHESLKGADRTSQRLEVLTPMTIRPDPPHREGQKLLHCEGRNVPVQOYL 266
QY 301 WEKEGVPPLKMTQBSALIFPFLNKSQGTGCTATSNMGSYKAYTTLNVNDPSPVPSS 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
267 WEKEGVPPLKMTQBSALIFPFLNKSQGTGCTATSNMGSYKAYTTLNVNDPSPVPSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYLTHKAGSDDDADDTAIIAEGG 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
327 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYLTHKAGSDDDADDTAIIAEGG 386
QY 421 QSGGDDKKEYFI 432
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
387 QSGGDDKKEYFI 398

RESULT 3

US-09-907-794A-84
; Sequence 84, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 15.8018 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPAAASLLLLLLPACCCWA.....A1NAEGSGGGDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	432	4	US-09-778-510-2
2	2059	90.9	398	4	US-09-778-510-6
3	2059	90.9	398	4	US-09-907-794A-84
4	2059	90.9	398	4	US-09-905-125A-84
5	2059	90.9	398	4	US-09-902-775A-84
6	1955	86.4	398	4	US-09-778-510-4
7	1189	52.5	227	4	US-09-205-258-947
8	1017.5	44.9	421	2	US-08-659-984A-1
9	1017.5	44.9	421	3	US-08-660-531-1
10	1017.5	44.9	444	2	US-08-659-984A-5
11	1017.5	44.9	444	3	US-08-660-531-5
12	723.5	32.0	440	4	US-09-866-028-61
13	722	31.9	442	4	US-09-778-510-20
14	722	31.9	442	4	US-09-930-803-1
15	715.5	31.6	423	4	US-09-778-510-22
16	342	15.1	65	4	US-09-205-258-949
17	319	14.1	58	4	US-09-205-258-950
18	317	14.0	64	4	US-09-205-258-948
19	310	13.7	64	4	US-09-205-258-361
20	280	12.4	52	4	US-09-205-258-951
21	249.5	11.0	393	1	US-08-423-742-2
22	242	10.7	388	1	US-08-423-742-4
23	239	10.6	517	4	US-09-723-368-4
24	238.5	10.5	503	4	US-08-999-689A-6
25	234	10.3	408	4	US-09-724-864-62
26	233	10.3	44	4	US-09-205-258-953
27	228.5	10.1	458	4	US-09-435-956A-1

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28 221.5 9.8 518 4 US-09-919-172-20
29 216.5 9.6 698 2 US-08-602-725-36
30 216.5 9.6 734 2 US-08-389-459A-17
31 216.5 9.6 734 3 US-08-987-867A-17
32 216.5 9.5 642 1 US-08-217-299-1
33 214.5 9.3 582 4 US-09-702-705-334
34 211.5 9.3 582 4 US-09-736-457-334
35 211.5 9.3 582 4 US-09-614-124B-334
36 211.5 9.3 582 4 US-09-671-325-334
37 211.5 9.3 582 4 US-09-589-184-334
38 210.5 9.3 583 2 US-08-432-016-2
39 210.5 9.3 583 2 US-08-684-594-2
40 209.5 9.3 479 4 US-09-723-368-2
41 208 9.2 338 2 US-08-414-657D-60
42 208 9.2 338 4 US-09-135-080-8
43 208 9.2 1651 3 US-09-540-245A-18
44 205.5 9.1 310 2 US-08-414-657D-45
45 205.5 9.1 338 2 US-08-414-657D-42

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ALIGNMENTS

RESULT 1

US-09-778-510-2

; Sequence 2, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US

; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: PCT/US99/17906

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/095,663

; PRIOR FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-778-510-2

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Query Match 100.0%; Score 2264; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 5.5e-196;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	51	ASQDSQPWTSDETVVAGT	VVVKQVQKHEDSSLOWNPACQOTLY	FGKRALRNRQLV	120
QY	121	TSTPHELSISINVALADEGEY	TCISFTMPVRTAKSLVTLVIGIPQKPI	ITGYKSSLRKD	180
DB	121	TSTPHELSISINVALADEGEY	TCISFTMPVRTAKSLVTLVIGIPQKPI	ITGYKSSLRKD	180
QY	181	TATLNCSSGSKPAARLTWRK	QDELGEPTQEDDNGKFTVSSSVTQVTR	EDDGAS	240
DB	181	TATLNCSSGSKPAARLTWRK	QDELGEPTQEDDNGKFTVSSSVTQVTR	EDDGAS	240
QY	241	IVCSVNHSLKGA	DRSTSQRIEVLVYTTAMRPPPHREGOK	LLHCEGRGNVPOOYL	300
DB	241	IVCSVNHSLKGA	DRSTSQRIEVLVYTTAMRPPPHREGOK	LLHCEGRGNVPOOYL	300
QY	301	WEKEGVPPLKMTQESAL	IFPFLNKS	DSGTGCTATSNMGSYKAYITLVNDP	SPVSSS
DB	301	WEKEGVPPLKMTQESAL	IFPFLNKS	DSGTGCTATSNMGSYKAYITLVNDP	SPVSSS